

# **PULLULANASE VARIANTS AND METHODS FOR PREPARING SUCH VARIANTS WITH PREDETERMINED PROPERTIES**

## **CROSS-REFERENCE TO RELATED APPLICATIONS**

5           This application is a division of US Application No. 09/514,599 filed February 28, 2000 and claims, under 35 U.S.C. 119, priority of Danish application no. PA 2000 00045 filed January 12, 2000, the contents of which are fully incorporated herein by reference.

## **FIELD OF THE INVENTION**

10   The present invention relates to variants of pullulanases and to methods for constructing such variants.

## **BACKGROUND OF THE INVENTION**

Starches such as corn, potato, wheat, manioc and rice starch are used as the starting material in commercial large scale production of sugars, such as high fructose syrup, high maltose syrup, maltodextrins, amylose, G4-G6 oligosaccharides and other carbohydrate products such as fat replacers.

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## **Degradation of starch**

Starch usually consists of about 80% amylopectin and 20% amylose. Amylopectin is a branched polysaccharide in which linear chains  $\Delta$ -1,4 D-glucose residues are joined by  $\Delta$ -1,6 glucosidic linkages. Amylopectin is partially degraded by  $\Delta$ -amylase, which hydrolyzes the 1,4- $\Delta$ -glucosidic linkages to produce branched and linear oligosaccharides. Prolonged degradation of amylopectin by  $\Delta$ -amylase results in the formation of so-called  $\Delta$ -limit dextrans which are not susceptible to further hydrolysis by the  $\Delta$ -amylase. Branched oligosaccharides can be hydrolyzed into linear oligosaccharides by a debranching enzyme. The remaining branched oligosaccharides

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can be depolymerized to D-glucose by glucoamylase, which hydrolyzes linear oligosaccharides into D-glucose.

Amylose is a linear polysaccharide built up of D-glucopyranose units linked together by  $\alpha$ -1,4 glucosidic linkages. Amylose is degraded into shorter linear oligosaccharides by  $\alpha$ -amylase, the linear oligosaccharides being depolymerized into D-glucose by glucoamylase.

In the case of converting starch into a sugar, the starch is depolymerized. The depolymerization process consists of a pretreatment step and two or three consecutive process steps, namely a liquefaction process, a saccharification process and, depending on the desired end product, optionally an isomerization process.

### **Pre-treatment of native starch**

Native starch consists of microscopic granules which are insoluble in water at room temperature. When an aqueous starch slurry is heated, the granules swell and eventually burst, dispersing the starch molecules into the solution. During this “gelatinization” process there is a dramatic increase in viscosity. As the solids level is 30-40% in a typical industrial process, the starch has to be thinned or “liquefied” so that it can be handled. This reduction in viscosity is today mostly obtained by enzymatic degradation.

### **Liquefaction**

During the liquefaction step, the long-chained starch is degraded into smaller branched and linear units (maltodextrins) by an  $\alpha$ -amylase (e.g. Termamyl™, available from Novo Nordisk A/S, Denmark). The liquefaction process is typically carried out at about 105-110°C for about 5 to 10 minutes followed by about 1-2 hours at about 95°C. The pH generally lies between about 5.5 and 6.2. In order to ensure an optimal enzyme stability under these conditions, calcium is added, e.g. 1 mM of calcium (40 ppm free calcium ions). After this treatment the liquefied starch will have a “dextrose equivalent” (DE) of 10-15.

## **Saccharification**

- After the liquefaction process the maltodextrins are converted into dextrose by addition of a glucoamylase (e.g. AMG™, available from Novo Nordisk A/S) and a debranching enzyme, such as an isoamylase (see e.g. US Patent No. 4,335,208) or a pullulanase (e.g. Promozyme®, available from Novo Nordisk A/S; see US Patent No. 4,560,651). Before this step the pH is reduced to a value below 4.5, e.g. about 3.8, maintaining the high temperature (above 95°C) for a period of e.g. about 30 min. to inactivate the liquefying  $\alpha$ -amylase to reduce the formation of short oligosaccharides called "panose precursors" which cannot be hydrolyzed properly by the debranching enzyme.
- 10 The temperature is then lowered to 60°C, glucoamylase and debranching enzyme are added, and the saccharification process proceeds for about 24-72 hours.

- Normally, when denaturing the  $\alpha$ -amylase after the liquefaction step, a small amount of the product comprises panose precursors which cannot be degraded by pullulanases or AMG. If active amylase from the liquefaction step is present during saccharification (i.e. no denaturing), this level can be as high as 1-2% or even higher, which is highly undesirable as it lowers the saccharification yield significantly. For this reason, it is also preferred that the  $\alpha$ -amylase is one which is capable of degrading the starch molecules into long, branched oligosaccharides (such as, e.g., the Fungamyl™-like  $\alpha$ -amylases) rather than shorter branched oligosaccharides.
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## **Isomerization**

- When the desired final sugar product is e.g. high fructose syrup, the dextrose syrup may be converted into fructose by enzymatic isomerization. After the saccharification process the pH is increased to a value in the range of 6-8, preferably about pH 7.5, and the calcium is removed by ion exchange. The dextrose syrup is then converted into high fructose syrup using, e.g., an immobilized glucose isomerase (such as Sweetzyme™, available from Novo Nordisk A/S).
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## **Debranching enzymes**

Debranching enzymes which can attack amylopectin are divided into two classes: isoamylases (E.C. 3.2.1.68) and pullulanases (E.C. 3.2.1.41), respectively. Isoamylase hydrolyses  $\alpha$ -1,6-D-glucosidic branch linkages in amylopectin and  $\beta$ -limit dextrins and can be distinguished from pullulanases by the inability of isoamylase to attack pullulan,  
5 and by their limited action on  $\alpha$ -limit dextrins.

When an acidic stabilized  $\alpha$ -amylase is used for the purpose of maintaining the amylase activity during the entire saccharification process (no inactivation), the degradation specificity should be taken into consideration. It is desirable in this regard to maintain the  $\alpha$ -amylase activity throughout the saccharification process, since this  
10 allows a reduction in the amyloglucidase addition, which is economically beneficial and reduces the AMG™ condensation product isomaltose, thereby increasing the DE (dextrose equivalent) yield.

It will be apparent from the above discussion that the known starch conversion processes are performed in a series of steps, due to the different requirements of the  
15 various enzymes in terms of e.g. temperature and pH. It would therefore be desirable to be able to engineer one or more of these enzymes, e.g. pullulanases, so that the overall process could be performed in a more economical and efficient manner. One possibility in this regard is to engineer the otherwise thermolabile pullulanases so as to render them more stable at higher temperatures.

## 20 **BRIEF DISCLOSURE OF THE INVENTION**

The inventors have modified the amino acid sequence of a pullulanase to obtain variants with improved properties, based on the three-dimensional structure of the pullulanase Promozyme® (available from Novo Nordisk A/S). The variants have altered physicochemical properties, e.g. an altered pH optimum, improved thermostability,  
25 increased specific activity or an altered cleavage pattern.

Accordingly, the object of the present invention is to provide a method for constructing pullulanases having altered properties, in particular to provide a method for constructing

pullulanases having improved thermostability, altered pH dependent activity and/or altered substrate specificity, such as increased isoamylase activity.

Thus, in its broadest aspect, the present invention relates to a method for constructing a variant of a parent pullulanase, wherein the variant has at least one altered property  
5 as compared to said parent pullulanase, which method comprises:

i) analyzing the structure of the pullulanase to identify, on the basis of an evaluation of structural considerations, at least one amino acid residue or at least one structural region of the pullulanase, which is of relevance for altering said property;

10 ii) constructing a variant of the pullulanase, which as compared to the parent pullulanase, has been modified in the amino acid residue or structural part identified in i) so as to alter said property; and

iii) testing the resulting pullulanase variant for said property.

The property which may be altered by the above methods of the present invention may be, e.g., thermostability, pH dependent activity, specific activity, or substrate specificity.  
15 Thus, the variant may have, e.g., increased thermostability, higher activity at a lower pH, an altered pH optimum, improved thermostability, or increased specific activity, such as increased isoamylase activity.

Although it has been described in the following that modification of the parent pullulanase in certain regions and/or positions is expected to confer a particular effect  
20 to the thus produced pullulanase variant (such as an improved thermostability or an increased isoamylase activity), it should be noted that modification of the parent pullulanase in any of such regions may also give rise to any other of the above-mentioned effects. For example, any of the regions and/or positions mentioned as being of particular interest with respect to, e.g., improved thermostability, may also give  
25 rise to, e.g., higher activity at a lower pH, an altered pH optimum, or increased specific activity, such as increased isoamylase activity.

Further aspects of the present invention relates to variants of a pullulanase, the DNA encoding such variants and methods of preparing the variants. Still further aspects of the present invention relates to the use of the variants for various industrial purposes, in particular for processes where sweeteners are made from starch. Other aspects of the present invention will be apparent from the below description as well as from the appended claims.

#### **BRIEF DESCRIPTION OF THE DRAWINGS**

Fig. 1 shows the DNA plasmid pCA36 harboring the gene encoding the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3).

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## DETAILED DISCLOSURE OF THE INVENTION

### Pullulanases

As explained above, pullulanases are enzymes classified in EC 3.2.1.41 and such enzymes are characterized by their ability to hydrolyze the  $\alpha$ -1,6-glycosidic bonds in, for example, amylopectin and pullulan.

A particularly interesting pullulanase is the pullulanase from *Bacillus acidopullulyticus* described in US 4,560,651 (hereinafter referred to as Promozyme®). Promozyme® has the amino acid sequence set forth in amino acids 1-921 of SEQ ID NO: 1. The three-dimensional structure of Promozyme® is described below.

Another interesting pullulanase is the pullulanase from *Bacillus deramificans* described in US 5,736,375. This enzyme has the amino acid sequence set forth in amino acid sequence 1-928 of SEQ ID NO: 3. Homology building of the three-dimensional structure of the above-mentioned pullulanase is described below.

In general, a preferred pullulanase suitable for the purpose described herein should have one or more of the following properties:

i) A three-dimensional structure homologous to Promozyme®.

ii) An amino acid sequence which is at least 40% homologous to SEQ ID NO:1 or SEQ ID NO:3, preferably at least 50%, e.g. at least 60%, such as at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% homologous to SEQ ID NO:1 or SEQ ID NO:3.

iii) A nucleic acid sequence which hybridizes to the nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:3.

The structural homology referred to above in i) above is based on other sequence homologies, hydrophobic cluster analysis or by reverse threading (Huber, T ; Torda, AE, PROTEIN SCIENCE Vol. 7 , No. 1 pp. 142-149 (1998)) and which by any of these

methods is predicted to have the same tertiary structure as Promozyme, wherein the tertiary structure refers to the overall folding or the folding of Domains N1, N2, A, B, and C. Alternatively, a structural alignment between Promozyme and homologous sequences may be used to identify equivalent positions.

- 5 For example, the homology between various pullulanase with known amino acid sequence has been compiled in the below matrix:

	1	2	3	4	5	6	7	8	9	10
1. pula_kleae	100	86	59	51	52	53	52	52	55	50
2. pula_klepn		100	58	51	51	53	53	53	53	52
10 3. w81973			100	55	56	52	55	54	51	56
4. r56989				100	98	60	76	54	56	76
5. sp929mat					100	61	78	54	57	78
6. fervido_x						100	61	57	54	62
7. sp734							100	56	54	91
15 8. r71616								100	54	56
9. w09257									100	54
10. Promozyme®										100

1. Pula\_kleae: Pullulanase from *Klebsiella aerogenes* (*J. Bacteriol.* (1987) **169**, 2301-2306).
- 20 2. Pula\_klepn: Pullulanase from *Klebsiella pneumonia* (*Mol. Microbiol.* (1990) **4**, 73-85; *J. Bacteriol.* (1985) **164**, 639-645; *J. Bacteriol.* (1989) **171**, 3673-3679).
3. W81973: Pullulanase fragment from zea mays (WO 98/50562).
4. r56989: Mature pullulanase from *Bacillus deramificans* T 89.117D (EP 0 605 040).
5. sp929mat: Mature part of pullulanase from *Bacillus deramificans* (US 5,736,375).
- 25 6. fervido\_x: Mature part of pullulanase from *Fervidobacterium pennavorans* Ven5 (*Appl. Environ. Microb.* (1997) **63**, 1088-1094).



7. sp734: Mature pullulanase from *Bacillus acidopullulyticus* (*FEMS Mic. Let.* (1994) **115**, 97-106.
8. r71616: Pullulanase from *Thermus sp.* (JP 07023783).
9. w09257: Pullulanase from *Bacillus sp.* KSM-AP 1378 (WO 96/35794).

The above homology calculations were determined by use of the GAP program from the UWGCG package using default values for GAP penalties, i.e. GAP creation penalty of 3.0 and GAP extension penalty of 0.1 (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711).

A sequence alignment between Promozyme® (SEQ ID NO: 1), the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) and the pullulanase from *Bacillus acidopullulyticus* (SEQ ID NO: 5) described in *FEMS Mic. Let.* (1994) **115**, 97-106, is shown in Appendix 2.

### **Three-dimensional structure of pullulanase**

Promozyme® was used to elucidate the three-dimensional structure forming the basis for the present invention.

The structure of Promozyme® was solved in accordance with the principle for x-ray crystallographic methods, for example, as given in X-Ray Structure Determination, Stout, G.K. and Jensen, L.H., John Wiley & Sons, Inc. NY, 1989.

The structural coordinates for the solved crystal structure of Promozyme® using the isomorphous replacement method are given in standard PDB format (Protein Data Bank, Brookhaven National Laboratory, Brookhaven, CT) as set forth in Appendix 1. It is to be understood that Appendix 1 forms part of the present application. In the context of Appendix 1, the following abbreviations are used: WAT refers to water or to calcium. Amino acid residues are given in their standard three letter code.

The structure of said Pullulanase is made up of five globular domains, ordered N1, N2, A, B, and C. The domains can be defined as being residues 1-310 for domain N1, 311-

420 for Domain N2, residues 421-556 and 596-835 for domain A, residues 557-595 for Domain B, residues 596-922 for Domain C, wherein the numbering refers to the amino acid sequence in SEQ ID NO: 1. Features of Domains N1, A, B and C of particular interest are described below.

## 5 Domain N1

Domain N1 contains in this particular pullulanase an extra loop of 100 residues compared to the pullulanase from *Bacillus acidopullulyticus* having the amino acid sequence shown in SEQ ID NO: 5. The loop is also present in the pullulanase from *Bacillus deramificans* having the amino acid sequence shown in SEQ ID NO: 3.

- 10 Part of the N2 domain is homologous to the N1 domain of Pseudomonase amyloclavata isoamylase (1bf2.pdb from Brookhaven database).

## Domain A

- 15 Domain A is the largest domain and contains the active site which comprises a cluster of three amino acid residues, D622, D736 and E651, spatially arranged at the bottom of a cleft in the surface of the enzyme. The structure of Domain A shows an overall fold in common with the  $\alpha$ -amylases for which the structure is known, viz. the (beta/alpha) 8 barrel with eight central beta strands (numbered 1-8) and eight flanking  $\alpha$ -helices. The  $\beta$ -barrel is defined by McGregor, *J. Prot. Chem.* 7:399, 1988. The C-terminal end of the beta strand 1 is connected to helix 1 by a loop denoted loop 1 and an identical pattern  
20 is found for the other loops, although the loops show some variation in size and some can be quite extensive.

- The eight central beta-strands in the (beta/alpha) 8 barrel superimpose reasonably well with the known structures of family 13 (Henrissat B. *Biochem. J.* (1991) **280**, 309-316 and Henrissat B. and Bairoch A. *Biochem. J.* (1993) **293**, 781-788). This part of the  
25 structure, including the close surroundings of the active site located at the C-terminal end of the beta-strands, shows a high degree of homology with isoamylases.

In contrast, the loops connecting the beta-strands and alpha helices display a high degree of variation from the known structures of family 13 enzymes. These loops constitute the structural context of the active site, and the majority of the contacts to the substrate is found among residues located in these loops. Distinguishing characteristics  
5 such as substrate specificity, substrate binding, pH activity profile, substrate cleavage pattern, and the like, are determined by specific amino acids and the positions they occupy in these loops.

### Domain B

Domain B, also referred to as loop 3 of the (beta/alpha) 8 barrel, in comprises amino  
10 acid residues 557-595 of the amino acid sequence shown in SEQ ID NO: 1. The most striking difference to other family 13 enzymes being the short amino acid sequence. This short sequence loop are of the same size as the isoamylase loop 3 and spatially positioned close to the active site residues and in close contact to the substrate.

### Domain C

15 Domain C in Promozyne comprises amino acid residues 596-922 of the amino acid sequence shown in SEQ ID NO: 1. Domain C is composed entirely of  $\beta$ -strands which form a single 8-stranded sheet structure that folds back on itself, and thus may be described as a  $\beta$ -sandwich structure. One part of the  $\beta$ -sheet forms the interface to Domain A.

### 20 Substrate Binding Site

Parts of the loop discussed above in the context of domains A, B and N2 are of particular interest for substrate interaction and active site reactivity. In particular, in domain A, residues 439-443 in loop 1, residues 490-514 in loop 2, residues 621-628 in loop 4, residues 652-668 in loop 5, residues 679-694 in loop 6, residues 733-740 in  
25 loop 7 and residues 787-796 in loop 8; in domain B, residues 553-564 and 581-592 in loop 3; in domain N2, residues 400-404, wherein residue positions correspond to the amino acids in the amino acid sequence in SEQ ID NO: 1.

### **Homology building of *Bacillus deramificans* pullulanase or other pullulanases.**

The structure of the *Bacillus deramificans* pullulanase (SEQ ID NO:3) was model built on the structure disclosed in Appendix 1 herein. The structure of other pullulanases may be built analogously.

- 5 A model structure of a pullulanase can be built using the Homology program or a comparable program, e.g., Modeller (both from Molecular Simulations, Inc., San Diego, CA). The principle is to align the sequence of the pullulanase with the known structure with that of the pullulanase for which a model structure is to be constructed. The structurally conserved regions can then be built on the basis of consensus sequences.
- 10 In areas lacking homology, loop structures can be inserted, or sequences can be deleted with subsequent bonding of the necessary residues using, e.g., the program Homology. Subsequent relaxing and optimization of the structure should be done using either Homology or another molecular simulation program, e.g., CHARMM from Molecular Simulations.

#### **15 Methods for designing novel pullulanase variants**

In a first aspect, the present invention relates to a method for producing a variant of a parent pullulanase, wherein the variant has at least one altered property as compared to the parent pullulanase, the method comprising:

- i) modeling the parent pullulanase on the three-dimensional structure of SEQ ID NO: 1 depicted in Appendix 1 to produce a three-dimensional structure of the parent pullulanase;
- ii) identifying in the three-dimensional structure obtained in step (i) at least one structural part of the parent pullulanase, wherein an alteration in the structural part is predicted to result in an altered property;
- 25 iii) modifying the nucleic acid sequence encoding the parent pullulanase to produce a nucleic acid sequence encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to the structural part; and

iv) expressing the modified nucleic acid sequence in a host cell to produce the variant pullulanase.

The structural part which is identified in step ii) of the method of the invention may be composed of one amino acid residue. Normally, however, the structural part comprises  
5 more than one amino acid residue, typically constituting one of the above-mentioned parts of the pullulanase structure such as one of the N1, N2, A, B, or C domains, an interface between any of these domains, a calcium binding site, a loop structure, the substrate binding site, or the like.

The structural or functional considerations may involve an analysis of the relevant  
10 structure or structural part and its contemplated impact on the function of the enzyme. For example, an analysis of the functional differences between pullulanases and the various isoamylases may be used for assigning certain properties of Promozyne® or homologous model builded structure to certain parts of the Promozyne® or homologous model builded structure or to contemplate such relationship. For instance,  
15 differences in the pattern or structure of loops surrounding the active site may result in differences in access to the active site of the substrate and thus differences in substrate specificity and/or cleavage pattern.

Furthermore, parts of a pullulanase involved in substrate binding, and thus, for example, substrate specificity and/or cleavage, thermostability, and the like, have been  
20 identified (*vide infra*).

The modification of an amino acid residue or structural region is typically accomplished by suitable modifications of a nucleic acid sequence encoding the parent enzyme in question. The modification may be substitution, deletion or insertion of an amino acid residue or a structural part.

25 The property to be modified may be stability (e.g. thermostability), pH dependent activity, substrate specificity, such as decreased condensation reactions, isoamylase like activity etc. Thus, the altered property may be an altered specific activity at a given

pH and/or altered substrate specificity, such as an altered pattern of substrate cleavage or an altered pattern of substrate inhibition.

In step ii) of the method according to the invention the part of the structure to be identified is preferably one which in the folded enzyme is believed to be in contact with the substrate (cf. the disclosure above in the section entitled "Substrate Binding Site") or involved in substrate specificity and/or cleavage pattern, and/or one which is contributing to the pH or temperature profile of the enzyme, or is otherwise responsible for the properties of the pullulanase.

Described in the following are specific types of variants which have been designed by use of the method of the invention.

The variants of the invention may comprise additional modifications in addition to the modifications described herein. The variants preferably have an amino acid sequence having more than 40% homology with SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5, preferably more than 50%, e.g. more than 60%, such as more than 70%, more than 75%, more than 80%, more than 85%, more than 90%, more than 91%, more than 92%, more than 93%, more than 94%, more than 95%, more than 96%, more than 97%, more than 98% or more than 99% homology with the amino acid sequences shown in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5.

In the present context the term "homologous to" or "homology" (also sometimes referred to as "similarity") is used in its conventional meaning and the "homology" between two amino acid sequences may be determined by use of any conventional algorithm, preferably by use of the GAP program from the UWGCG package using default values for GAP penalties, i.e. GAP creation penalty of 3.0 and GAP extension penalty of 0.1 (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711). The method is also described in S.B. Needleman and C.D. Wunsch, *Journal of Molecular Biology*, **48**, 443-445 (1970).

As mentioned above, the property to be modified may be stability (e.g. thermostability), pH dependent activity, substrate specificity, such as increased isoamylase activity, or specific activity. Thus, the altered property may be an altered specific activity at a given pH and/or an altered substrate specificity, such as an altered pattern of substrate  
5 cleavage or an altered pattern of substrate inhibition.

In a particular interesting embodiment of the invention the property to be modified is the thermostability of the enzyme.

In the present context, the term "thermostable" (or "thermostability") refers in general to the fact that the pullulanase variants according to the invention have an improved  
10 thermostability compared to the relevant parent pullulanase. The degree of improvement in thermostability can vary according to factors such as the thermostability of the parent pullulanase and the intended use of the pullulanase variant, i.e. whether it is primarily intended to be used for liquefaction or for saccharification or both. It will be apparent from the discussion below that for saccharification, the enzyme variant should  
15 maintain a substantial degree of enzyme activity during the saccharification step at a temperature of at least about 63°C, preferably at least about 70°C, while an enzyme variant designed for use in the liquefaction step should be able to maintain a substantial degree of enzyme activity at a temperature of at least about 95°C.

The improved thermostability of enzyme variants according to the invention can in  
20 particular be defined according to one or more of the following criteria:

In one embodiment, the pullulanase variant of the invention has an improved thermostability (and/or the method of the invention provides a pullulanase with an improved thermostability) as defined by differential scanning calorimetry (DSC) using the method described herein.

25 In another embodiment, the pullulanase variant of the invention has an improved thermostability (and/or the method of the invention provides a pullulanase with an improved thermostability) as defined by an increased half-time ( $T_{1/2}$ ) of at least about 5%, preferably at least about 10%, more preferably at least about 15%, more preferably

at least about 25%, most preferably at least about 50%, such as at least about 100%, in the "T<sub>1/2</sub> assay for liquefaction" described herein, using a pH of 5.0 and a temperature of 95°C. Pullulanase variants according to this definition are suitable for use in the liquefaction step of the starch conversion process.

- 5 Alternatively or additionally, a pullulanase variant suitable for use in liquefaction can be defined as having an improved thermostability as defined by an increased residual enzyme activity of at least about 5%, preferably at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the "assay for residual activity after liquefaction"
- 10 described herein, using a pH of 5.0 and a temperature of 95°C.

In a further embodiment, the enzyme variant of the invention has an improved thermostability (and/or the method of the invention provides a pullulanase with an improved thermostability) as defined by an increased half-time (T<sub>1/2</sub>) of at least about 5%, preferably at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in

15 the "T<sub>1/2</sub> assay for saccharification" described herein, using a pH of 4.5 and a temperature of 70°C. Such variants are suitable for use in the saccharification step of the starch conversion process.

- Alternatively or additionally, a pullulanase variant suitable for saccharification can be
- 20 defined as having an improved thermostability as defined by an increased residual enzyme activity of at least about 5%, preferably at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the "assay for residual activity after saccharification" described herein, using a pH of 4.5 and a temperature of 63°C.
- 25 Preferably, this improved thermostability is also observed when assayed at a temperature of 70°C.

The term "substantially active" as used herein for a given pullulanase variant and a given set of conditions of temperature, pH and time means that the relative enzymatic



activity of the enzyme variant is at least about 25%, preferably at least about 50%, in particular at least about 60%, especially at least about 70%, such as at least about 90% or 95%, e.g. at least about 99% compared to the relative activity of the parent enzyme tested under the same set of conditions.

- 5 One advantage of the thermostable pullulanase of the invention is that they make it possible to perform liquefaction and debranching simultaneously before the saccharification step. This has not previously been possible, since the known pullulanases with acceptable specific activity are thermolabile and are inactivated at temperatures above 60°C. (Some thermostable pullulanases from *Pyrococcus* are
- 10 known, but these have an extremely low specific activity at higher temperatures and are thus unsuitable for purposes of the present invention). By debranching, using the thermostable pullulanases of the invention, during liquefaction together with the action of an  $\alpha$ -amylase, the formation of panose precursors is reduced, thereby reducing the panose content in the final product and increasing the overall saccharification yield. It is
- 15 also possible in this manner to extend the liquefaction process time without risking formation of large amount of panose precursors. By prolonging the liquefaction step, the DE yield is increased from 10-15 to e.g. 15-20, reducing the need for glucoamylase. This reduced glucoamylase requirement is in turn advantageous as the formation of undesired isomaltose is reduced, thereby resulting in an increased glucose yield. In
- 20 addition, the reduced glucoamylase addition enables the saccharification step to be carried out at a higher substrate concentration (higher DS, dry substances, concentration) than the normal approx. 30-35% used according to the prior art. This allows reduced evaporation costs downstream, e.g. in a high fructose corn syrup process, and the saccharification reaction time can also be reduced, thereby increasing
- 25 production capacity. A further advantage is that  $\alpha$ -amylase used in the liquefaction process does not need to be inactivated/denatured in this case.

Furthermore, it is also possible to use the thermostable pullulanases of the invention during saccharification, which is advantageous for several reasons. In the conventional starch saccharification process, the process temperature is not more than 60°C due to

30 the fact that neither the saccharification enzyme pullulanase nor AMG™ are sufficiently

thermostable to allow the use of a higher temperature. This is a disadvantage, however, as it would be very desirable to run the process at a temperature of above about 60°C, in particular above 63°C, e.g. about 70°C, to reduce microbial growth during the relatively long saccharification step. Furthermore, a higher process temperature normally gives a  
5 higher activity per mg of enzyme (higher specific activity), thereby making it possible to reduce the weight amount of enzyme used and/or obtain a higher total enzymatic activity. A higher temperature can also result in a higher dry matter content after saccharification, which would be beneficial in terms of reducing evaporation costs.

In another interesting embodiment of the invention the property to be modified is the  
10 substrate specificity of the pullulanase, in particular to modify the substrate specificity of the pullulanase in such a way the variant pullulanase becomes more "isoamylase-like" in the sense of having an increased activity towards high molecular weight branched starchy material such as glycogen and amylopectin. Methods for determining the substrate specificity of pullulanases are discussed in the following section entitled  
15 "Methods for determining stability, activity and specificity".

Thus, when used herein, the term "increased isoamylase activity" refers in general to the fact that the pullulanase variants according to the invention exhibits a higher activity towards high molecular weight branched starchy material, such as glycogen and amylopectin as compared to the parent pullulanase.

20 The increased isoamylase activity of the pullulanase variants according to the invention can in particular be defined according to the below criteria:

In one embodiment the pullulanase variant according to the invention has an increased isoamylase activity as defined by an increase of at least 5%, preferably of at least 10%, more preferably of at least 15%, more preferably of at least 25%, most preferably of at  
25 least 50%, in particular of at least 75%, such as of at least 100% in the number of reducing ends formed in the "assay for isoamylase-like activity" described herein, using 50 mM sodium acetate, a pH of 4.5, 5.0 or 5.5, a temperature of 60°C and when incubated with a 10 w/v rabbit liver glycogen solution for a period of 10 min.

In the present context the term “pullulanase activity” is intended to mean that the pullulanase variant in question is capable of degrading pullulan when tested as described in the Examples (see the section entitled “Determination of pullulanase activity”).

## 5 **Methods for determining stability, activity and specificity**

### Thermostability

Thermostability of pullulanases can be detected by measuring the residual activity by incubating the enzyme under accelerated stress conditions, which comprise: pH 4.5 in a 50 mM sodium acetate buffer without a stabilizing dextrin matrix (such as the approximately 35% dry matter which is normally present during saccharification). The stability can be determined at isotherms of e.g. 63°C, 70°C, 80°C, 90°C and 95°C, measuring the residual activity of samples taken from a water bath at regular intervals (e.g. every 5 or 10 min.) during a time period of 1 hour. For determining stability for the purpose of liquefaction, a pH of 5.0, a temperature of 95°C and a total assay time of 30 to 120 minutes are used (“assay for residual activity after liquefaction”). For determining stability for the purpose of saccharification, a pH of 4.5, a temperature of 63°C or 70°C and a total assay time of 30 minutes are used (“assay for residual activity after saccharification”).

Alternatively, the thermostability may be expressed as a “half-time” ( $T_{1/2}$ ), which is defined as the time, under a given set of conditions, at which the activity of the enzyme being assayed is reduced to 50% of the initial activity at the beginning of the assay. In this case, the “ $T_{1/2}$  assay for liquefaction” uses a pH of 5.0 and a temperature of 95°C, while the “ $T_{1/2}$  assay for saccharification” uses a pH of 4.5 and a temperature of 70°C. The assay is otherwise performed as described above for the respective assays for residual activity.

### Activity: Somogyi-Nelson method for determination of reducing sugars

The activity of pullulanases can be measured using the Somogyi-Nelson method for the determination of reducing sugars (*J. Biol. Chem.* **153**, 375 (1944)). This method is based on the principle that sugar reduces cupric ions to cuprous oxide, which reacts with an arsenate molybdate reagent to produce a blue colour that is measured  
 5 spectrophotometrically. The solution to be measured must contain 50-600 mg of glucose per liter. The procedure for the Somogyi-Nelson method is as follows:

Sample value: Pipet 1 ml of sugar solution into a test tube. Add 1 ml of copper reagent. Stopper the test tube with a glass bead. Place the test tube in a boiling water bath for 20 minutes. Cool the test tube. Add 1 ml of Nelson's color reagent. Shake the test tube  
 10 without inverting it. Add 10 ml of de-ionized water. Invert the test tube and shake vigorously. Measure the absorbance at 520 nm, inverting the test tube once immediately prior to transfer of the liquid to the cuvette.

Blank value: Same procedure as for the sample value, but with water instead of sugar solution.

15 Standard value: Same procedure as for the sample value.

Calculations: In the region 0-2 the absorbance is proportional to the amount of sugar.

$$20 \quad \text{mg sugar/l} = \frac{100 (\text{sample} - \text{blank})}{(\text{standard} - \text{blank})}$$

$$25 \quad \% \text{ glucose} = \frac{(\text{sample} - \text{blank})}{100 \times (\text{standard} - \text{blank})}$$

## Reagents:

### 1. Somogyi's copper reagent

35.1 g  $\text{Na}_2\text{HPO}_4 \cdot 2\text{H}_2\text{O}$  and 40.0 g potassium sodium tartrate ( $\text{KNaC}_4\text{H}_4\text{O}_6 \cdot 4\text{H}_2\text{O}$ ) are dissolved in 700 ml of de-ionized water. 100 ml of 1N sodium hydroxide and 80 ml of 10% cupric sulphate ( $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ ) are added. 180 g of anhydrous sodium sulphate are dissolved in the mixture, and the volume is brought to 1 liter with de-ionized water.

### 2. Nelson's color reagent

50 g of ammonium molybdate are dissolved in 900 ml of de-ionized water. Then 42 ml of concentrated sulphuric acid are added, followed by 6 g of disodium hydrogen arsenate heptahydrate dissolved in 50 ml of deionized water, and the volume is brought to 1 litre with deionized water. The solution is allowed to stand for 24-48 hours at 37°C before use and is stored in the dark in a brown glass bottle with a glass stopper.

### 3. Standard

100 mg of glucose (anhydrous) are dissolved in 1 liter of de-ionized water.

Alternatively, the release of reducing sugars can be measured using a 96 well plate set-up modified after Fox, J.D. & Robyt, J.F. (1991) Anal. Biochem. 195, 93-96. Assay conditions are (in brief): 1 ml substrate (e.g. 1% solution) in 50 mM citric acid pH 5 is preincubated at 60 °C. A zero timepoint is taken 150 µl sample and transferred to a microtiter plate well containing 150 µl solution A + B for reducing sugar determination. The enzymatic reaction is initiated by addition of 100 µl enzyme and time points are taken at T = 1, 2, 3, 4, and 5 min.

After completion of the assay, the plate is developed by incubation at 85 °C for 70 minutes and the plate is read at 540 nm.

Reagents for determination of reducing value: Solution A) and solution B (62 mg copper sulfate pentahydrate and 63 mg L-serine in 50 ml water).

### Pullulanase specificity

Methods for the determination and characterization of the profile of action and specificity of pullulanases for various substrates (e.g. amylopectin, glycogen and pullulan) are described by Kainuma et al. in *Carbohydrate Research*, **61** 345-357 (1978). Using these methods, the relative activity of a pullulanase can be determined, and the relative activity of a pullulanase variant according to the invention compared to the relative activity of the parent pullulanase can be assessed, for example to determine whether a pullulanase variant has the desired increased specificity toward high molecular weight saccharides, such as amylopectin, compared to the parent pullulanase.

In order to determine whether the pullulanase variant possesses an increased isoamylase activity as compared to the parent pullulanase the following test may be performed ("assay for isoamylase-like activity"):

1000 mg rabbit liver glycogen is dissolved in 40 ml water to which 0.2% NaOH has been added. 800 mg NaBH<sub>4</sub> is added carefully under stirring. The solution is stirred for 48 hours at 25°C after which the reaction is stopped by addition of Amberlite IR-118H (a cation exchanger which removes the boron ions and hence stops the reaction). The solution is filtered to remove the matrix and evaporated to give 10 ml. The solution is then dialyzed extensively against de-ionized water to remove residual boron ions. The parent pullulanase and the pullulanase variant are assayed according to the method of Somogyi-Nelson, using 50 mM sodium acetate, pH values of 4.5, 5.0 or 5.5 and a temperature of 60°C, with a reaction time of 10 minutes. Glucose is used as a standard, a standard curve being made from solutions containing of 0-200 mg glucose/liter.

Clearly, the higher the number of reducing ends formed during the incubation period, the higher "isoamylase activity". The increase in the pullulanase variant's isoamylase activity is expressed as a percentage value based on the original "isoamylase activity" of the parent pullulanase.

### Pullulanase variants with altered stability

A variant with improved stability (typically increased thermostability) may be obtained by substitution with proline, substitution of histidine with another amino acid, introduction of a disulfide bond, removal of a deamidation site, altering a hydrogen bond contact, filling  
5 in an internal structural cavity with one or more amino acids with bulkier side groups, introduction of interdomain interactions, altering charge distribution, helix capping, or introduction of a salt bridge.

#### Increased mobility regions:

The following regions have an increased mobility in the crystal structure of  
10 Promozyme®, and it is presently believed that these regions can be responsible for stability or activity of the enzyme. Improvements of the enzyme can be obtained by mutation in the below regions and positions. Introducing e.g. larger residues or residues having more atoms in the side chain could increase the stability, or e.g. introduction of residues having fewer atoms in the side chain could be important for the mobility and  
15 thus the activity profile of the enzyme. The regions can be found by analysing the B-factors taken from the pdb file, and/or from molecular dynamics calculations of the isotropic fluctuations. These can be obtained by using the program CHARMM from MSI (Molecular simulations inc.).

Thus, in order to stabilize mobile regions in the structure, a preferred variant of a parent  
20 pullulanase comprises a modification, e.g. a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

408-429 (i.e. 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428 and 429),

25 300-314 (i.e. 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313 and 314),

157-165 (i.e. 157, 158, 159, 160, 161, 162, 163, 164 and 165),

95-113 (i.e. 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112 and 113),

130-140 (i.e. 130, 131, 132, 133, 134, 135, 136, 137, 138, 139 and 140),

232-238 (i.e. 232, 233, 234, 235, 236, 237 and 238),

5 266-272 (i.e. 266, 267, 268, 269, 270, 271 and 272),

302-308 (i.e. 302, 303, 304, 305, 306, 307 and 308),

418-428 (i.e. 418, 419, 420, 421, 422, 423, 424, 425, 426, 427 and 428),

500-507 (i.e. 500, 501, 502, 503, 504, 505, 506 and 507),

659-665 (i.e. 659, 660, 661, 662, 663, 664 and 665) and

10 751-755 (i.e. 751, 752, 753, 754 and 755).

Similar modifications, e.g. substitutions, may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, other preferred modifications, e.g. substitutions, which are believed to  
15 stabilized mobile regions in the structure of the pullulanase from *Bacillus deramificans*, correspond to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 3:

406-427 (i.e. 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426 and 427),

20 298-312 (i.e. 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311 and 312),

153-161 (i.e. 153, 154, 155, 156, 157, 158, 159, 160 and 161),



91-109 (i.e. 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108 and 109),

126-136 (i.e. 126, 127, 128, 129, 130, 131, 132, 133, 134, 135 and 136),

5

230-236 (i.e. 230, 231, 232, 233, 234, 235 and 236),

264-270 (i.e. 264, 265, 266, 267, 268, 269 and 270),

10 300-306 (i.e. 300, 301, 302, 303, 304, 305 and 306),

416-426 (i.e. 416, 417, 418, 419, 420, 421, 422, 423, 424, 425 and 426),

498-505 (498, 499, 500, 501, 502, 503, 504 and 505),

15

656-662 (i.e. 656, 657, 658, 659, 660, 661 and 662) and

749-753 (i.e. 749, 750, 751, 752 and 753).

20 Furthermore, it is envisaged from the structure that deletion of certain amino acid residues will confer increased stability, such as increased thermostability, to the thus produced variant. Variants, which are believed to be of particular importance, comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

25 Deletion of the peptide fragment 158-275, such as a deletion starting from position 158, 159, 160 or 161 and ending at position 270, 271, 272, 273, 274 or 275, i.e. the longest deletion will be deletion of the peptide fragment 158-275 and the shortest deletion will be deletion of the peptide fragment 161-270.

Other deletions which are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

- 5 Deletion of the peptide fragment 1-315, such as deletion of the peptide fragment 1-314, 1-313, 1-312, 1-311, 1-310, 1-309, 1-308, 1-307, 1-306, 1-305, or 1-304.

Furthermore, the following deletions are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth

- 10 in SEQ ID NO: 1:

Deletion of the peptide fragment 1-115, such as deletion of the peptide fragment 1-114, 1-113, 1-112, 1-111, 1-110, 1-109, 1-108, 1-107, 1-106 or 1-105.

Similar deletions may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any

- 15 of the other modifications disclosed herein.

For example, it is envisaged that deletion of the below amino acid residues will confer increased stability, such as increased thermostability, to the thus produced variant of the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3):

- 20 Deletion of the peptide fragment 154-273, such as a deletion starting from position 154, 155, 156 or 157 and ending at position 268, 269, 270, 271, 272 or 273, i.e. the longest deletion will be deletion of the peptide fragment 154-273 and the shortest deletion will be deletion of the peptide fragment 157-268.

- Other deletions which are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino acid residues  
25 corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 3:

Deletion of the peptide fragment 1-313, such as deletion of the peptide fragment 1-312, 1-311, 1-310, 1-309, 1-308, 1-307, 1-306, 1-305, 1-304, or 1-303.

Furthermore, the following deletions are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino acid  
5 residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 3:

Deletion of the peptide fragment 1-111, such as deletion of the peptide fragment 1-111, 1-110, 1-109, 1-108, 1-107, 1-106, 1-105, 1-104, 1-103, 1-102 or 1-101.

### Cavities and crevices

10 The structure of the pullulanase contains a number of unique internal cavities, which may contain water, and a number of crevices. In order to increase the stability, preferably the thermostability, of the pullulanase it may be desirable to reduce the number or size of cavities and crevices, e.g., by introducing one or more hydrophobic contacts, preferably achieved by introducing amino acids with bulkier side chains in the  
15 vicinity or surroundings of the cavity or crevice. For instance, the amino acid residues to be modified are those which are involved in the formation of a cavity or crevice.

In order to determine which amino acid residues of a given enzyme are involved in the formation of cavities or crevices the Connolly program is normally used (B. Lee and F.M. Richards, *J. Mol. Biol.* **55**, 379-400 (1971)). The program uses a probe with a certain  
20 radius to search the external and internal surface of the protein. The smallest crevice observable in this way has the probe radius.

To analyze the solved structure of Promozyne®, a modified version of the Connolly program included in the program of INSIGHT was used. In the first step, the water molecules and the ions were removed by unmerging these atoms from the solved struc-  
25 ture. By using the command MOLECULE SURFACE SOLVENT the solvent accessible surface area was calculated for all atoms and residues using a probe radius of 1.4 Å, and displayed graphically together with the model of the solved structure. The internal cavities are then seen as dot surfaces with no connections to the external surface.

Suggestions for specific modifications to fill out the cavities are given below. By using the homology built structures and/or comparisons based on sequence alignment, mutations for homologous structures of pullulanases can be made.

Accordingly, in a further aspect the present invention relates to a method for  
5 constructing a variant of a parent pullulanase, the method comprising:

a) identifying an internal cavity or crevice in the three-dimensional structure of the parent pullulanase;

b) substituting at least one amino acid residue involved in the formation of a cavity or crevice with another amino acid residue which increases the hydrophobic interaction and/or fills out or reduces the size of the cavity or crevice;

c) optionally repeating steps a) and b) recursively;

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);

e) preparing the variant resulting from steps a) - d);

f) testing the stability and/or the temperature dependent activity profile of the variant; and

g) optionally repeating steps a) - f) recursively; and

h) selecting a variant having increased stability and/or an altered temperature dependent activity profile as compared to the parent pullulanase.

In a preferred embodiment of the invention the variant pullulanase provided by the above method have increased thermostability as compared to the parent pullulanase. The thermostability of a given variant may be assessed as described in the above section entitled "Methods for determining stability, activity and specificity".

It will be understood that the cavity or crevice is identified by the amino acid residues surrounding said cavity or crevice, and that modification of said amino acid residues are of importance for filling or reducing the size of the cavity or crevice. Preferably, the modification is a substitution with a bulkier amino acid residue, i.e. one with a greater side chain volume or with an increased number of atoms in the side chain. For example, all the amino acids are bulkier than Gly, whereas Tyr and Trp are bulkier than Phe. The particular amino acid residues referred to below are those which in a crystal structure have been found to flank the cavity or crevice in question.

In a preferred embodiment, the variant of a pullulanase, in order to fill, either completely or partly, cavities or crevices located internally or externally in the structure, comprises a modification, e.g. a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

406, 394, 568, 573 576, 563, 557, 396, 392, 515, 583, 442, 792, 767, 732, 760, 783, 740, 688, 478, 534, 550, 627, 314.

In a more preferred embodiment, the variant of a pullulanase comprises one or more substitutions corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 1:

G406A, P394F/W/I/L, I568L/F, Y573W, T576N/L/I, S563T, T557N, A396V/L/I, V392, N515M/L/I, V583I/F/L, D442Q, S792Y/F, V767Q/E/L/I, V732I/L, D760Q/E/F/Y, L783F/Y, L740Q, D688Y/F/E/Q/R/K, L478Q/R, L534F/Y/I, M550F/Y/I/L, L627F/Y/I, L314I.

Similar modifications, e.g. substitutions, may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, the variant of a pullulanase may also comprise one or more substitutions corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 3:

566, 485, 487, 437, 775, 779, 551, 428, 492, 495, 392, 621, 437+503, 674+664 and 823.

In a more preferred embodiment, the variant of a pullulanase comprises one or more substitutions corresponding to the following substitutions in the amino acid sequence  
5 set forth in SEQ ID NO: 3:

I566A, Q485H, M487L, D437H, Q775H, E779D, V551I, I428Y/F, S492F, V495I/F/Y, P392Y, L621Q, D437H+D503Y, V674+L664F and L823V.

### Disulfide bonds

10 A variant with improved stability (typically improved thermostability) as compared to the parent pullulanase may be obtained by introducing new interdomain and intradomain contacts, such as establishing inter- or intradomain disulfide bridges.

Accordingly, a further aspect of the present invention relates to a method for constructing a variant of a parent pullulanase, the method comprising:

- 15 a) identifying in the three-dimensional structure of the parent pullulanase two or more amino acid residues which, when substituted with cysteines, are capable of forming a disulfide bond;
- b) substituting the amino acids identified in a) with cysteines;
- c) optionally repeating steps a) and b) recursively;
- 20 d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);
- e) preparing the variant resulting from steps a) - d);
- f) testing the stability of said variant; and
- g) optionally repeating steps a) - f) recursively; and

h) selecting a variant having increased stability as compared to the parent pullulanase.

In a preferred embodiment of the invention the variant pullulanase provided by the above method have increased thermostability as compared to the parent pullulanase. The  
5 thermostability of a given variant may be assessed as described in the above section entitled "Methods for determining stability, activity and specificity".

In order to determine, in the three-dimensional structure of the parent pullulanase, the amino acid residues which, when substituted with cysteines, are capable of forming a disulfide bond, residues with CB atoms less than 4Å from each other, and where the  
10 direction of the CA-CB from each residue is pointing towards the other residue are identified. Following the above-mentioned guidelines, the below amino acid residues were identified in the amino acid sequence of SEQ ID NO: 1, and it is contemplated that these residues are suitable for cysteine replacement, thereby opening up the possibility of establishing one or more disulfide bridges in the variant pullulanase:

15 K758C+I914C, T916C+A765C, I897C+S819C, P525C+E499C, H286C+T148C.

Similar substitutions may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, it is contemplated that the following residues, identified in the amino acid  
20 sequence of the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3), are suitable for cysteine replacement, thereby opening up the possibility of establishing one or more disulfide bridges in the variant pullulanase:

K756C/I912C, M914C/A763C, V895C/G817C, A523C/E497C, H284C/T144C.

#### Surface charge distribution

25 A variant with improved stability (typically improved thermostability) as compared to the parent pullulanase may be obtained by changing the surface charge distribution of the

pullulanase. For example, when the pH is lowered to about 5 or below histidine residues typically become positively charged and, consequently, unfavorable electrostatic interactions on the protein surface may occur. By engineering the surface charge of the pullulanase one may avoid such unfavorable electrostatic interactions  
5 which in turn leads to a higher stability of the pullulanase.

Therefore, a further aspect of the present invention relates to method for constructing a variant of a parent pullulanase, the method comprising:

- a) identifying, on the surface of the parent pullulanase, at least one amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His;
- 10 b) substituting, on the surface of the parent pullulanase, at least one amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His with an uncharged amino acid residue;
- c) optionally repeating steps a) and b) recursively;
- 15 d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);
- e) preparing the variant resulting from steps a) - d);
- f) testing the stability of said variant; and
- g) optionally repeating steps a) - f) recursively; and
- h) selecting a variant having increased stability as compared to the parent  
20 pullulanase.

As will be understood by the skilled person it may also, in some cases, be advantageous to substitute an uncharged amino acid residue with an amino acid residue bearing a charge or, alternatively, it may in some cases be advantageous to substitute an amino acid residue bearing a charge with an amino acid residue bearing a  
25 charge of opposite sign. Thus, the above-mentioned method may easily be employed



by the skilled person also for these purposes. In the case of substituting an uncharged amino acid residue with an amino acid residue bearing a charge the above-mentioned method may be employed the only difference being steps a) and b) which will then read:

5 a) identifying, on the surface of the parent pullulanase, at least one uncharged amino acid residue;

b) substituting, on the surface of the parent pullulanase, at least one uncharged amino acid residue with a charged amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His.

10 Also in the case of changing the sign of an amino acid residue present on the surface of the pullulanase the above method may be employed. Again, compared to the above method, the only difference being steps a) and b) which, in this case, read:

a) identifying, on the surface of the parent pullulanase, at least one charged amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His;

15 b) substituting, on the surface of the parent pullulanase, at least one charged amino acid residue identified in step a) with an amino acid residue having an opposite charge.

Thus, Asp may be substituted with Arg, Lys or His; Glu may be substituted with Arg, Lys or His; Arg may be substituted with Asp or Glu; Lys may be substituted with Asp or Glu; and His may be substituted with Asp or Glu.

20 In a preferred embodiment of the invention the variant pullulanase provided by the above method(s) have increased thermostability as compared to the parent pullulanase. The thermostability of a given variant may be assessed as described in the above section entitled "Methods for determining stability, activity and specificity".

In order to determine the amino acid residues of a pullulanase, which are present on  
25 the surface of the enzyme, the surface accessible area are measured using the DSSP

program (Kabsch and Sander, *Biopolymers* (1983), **22**, 2577-2637). All residues having a surface accessibility higher than 0 is regarded a surface residue.

The amino acid residues found on the surface of Promozyme® using the above method are as follows:

5 E526, Q544, E760, N338, N228, N181,

and it is contemplated that the following substitutions are of particular interest:

E526H, Q544E, E760Q, N338K/R, N228DE/, N181K/R.

Similar substitutions may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any  
10 of the other modifications disclosed herein.

For example, the variant of a pullulanase may also comprise one or more modifications, e.g. substitutions, corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 3:

444, 530, 710 and 855.

15 In a more preferred embodiment, the variant of a pullulanase comprises one or more substitutions corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 3:

D444R/K, K530Y/F/L, N710R and T855K.

#### Other modifications

20 Variants with improved stability, in particular variants with improved thermostability, can be obtained by improving existing or introducing new interdomain or intradomain contacts. Such improved stability can be achieved by the modifications listed below.

Thus, one preferred embodiment of the invention relates to a variant of a parent pullulanase which has an improved stability and one or more salt bridges as compared

to the parent pullulanase, wherein said variant comprises a modifications, e.g. a substitution, in a position corresponding to at least one of the following sets of positions in SEQ ID NO: 1:

301, 385, 298, 299, 385 and 299+385, in particular L301R, N385R, H298R, N299R,  
5 N385D and N299R+N385D.

Similar modifications, e.g. substitutions, may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, it is contemplated that the following substitutions in the pullulanase  
10 having the amino acid sequence set forth in SEQ ID NO: 3 will enhance the stability of the enzyme: T891D, S892K, T891D+S892K and N400R.

In another preferred embodiment, the variant of the pullulanase comprises a substitution corresponding to one or more of the following substitutions with proline in the amino acid sequence set forth in SEQ ID NO: 1:

15 G293P, K151P, K122P, N315P, N374P, N793P, A446P, G672P, G668P, T556P

In a further interesting embodiment of the invention, the variant of the pullulanase comprises a substitution corresponding to one or more of the following substitutions with proline in the amino acid sequence set forth in SEQ ID NO: 3:

D562P, G794P, G292P, D148P, N119P, D314P, N373P, N792P, G671P, G667P and  
20 T554P.

Analogously, it may be preferred that one or more histidine residue(s) present in the parent pullulanase is (are) substituted with a non-histidine residues such as Y, V I, L, F, M, E, Q, N, or D. Accordingly, in another preferred embodiment, the variant of the parent pullulanase comprises a substitution of an amino acid residue corresponding to  
25 one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 3: H422Y/F/L, H483Y/F/L, H543Y/F/L/N and H613Y/F/L.

It may be preferred that one or more asparagine or glutamine residues present in the parent pullulanase is or are substituted with a residue lacking the amide group on the side chain. Preferably, such asparagines or glutamine residues are substituted with S, T, V, L and/or F amino acid residues. Accordingly, in another preferred embodiment, 5 the variant of the parent pullulanase comprises a modification, e.g. a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

Q543, Q339, N337, Q380, Q353, N384, N286, N298, N227, Q227, Q210, N180, Q259, N583, N790, N793, N505, N788, N736, N684, N689 or N681, preferably 10 Q543S/T/V/L/F, Q339S/T/V/L/F, N337S/T/V/L/F, Q380S/T/V/L/F, Q353S/T/V/L/F, N384S/T/V/L/F, N286S/T/V/L/F, N298S/T/V/L/F, N227S/T/V/L/F, Q227S/T/V/L/F, Q210S/T/V/L/F, N180S/T/V/L/F, Q259S/T/V/L/F, N583S/T/V/L/F, N790S/T/V/L/F, N793S/T/V/L/F, N505S/T/V/L/F, N788S/T/V/L/F, N736S/T/V/L/F, N684S/T/V/L/F, N689S/T/V/L/F and N681S/T/V/L/F.

15 The corresponding residues found in the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) include:

N400, N446, N504, N717, N735 and N789, preferably N400S/T/V/L/F, N446S/T/V/L/F, N504S/T/V/L/F, N717S/T/V/L/F, N735S/T/V/L/F and N789S/T/V/L/F.

Moreover, it is contemplated that modifications, e.g. substitutions, in the region linking 20 the N2 and the A domain, as well as other regions linking other domains, will confer additional stability, such as an increased thermostability, to the enzyme. Thus, in an interesting embodiment of the invention, the pullulanase variant comprises one or more modifications, e.g. substitutions, in the domain-linking regions (e.g. the region linking the N2 and A domains).

25 Examples of such modifications include one or more of the following substitutions in the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3):

111, 112,

158-160 (i.e. 158, 159 and 160),

270-274 (i.e. 270, 271, 272, 273 and 274),

302-314 (i.e. 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313 and 314) and

408-426 (i.e. 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421,

5 422, 423, 424, 425 and 426).

Examples of specific substitutions are: S111T/V/L, N112S/T/Q, S158Y/F/T, L159Y/K/R/A/S/T, G160A/S/T, D270E/S/T, L271V/I, V272I, T273N/D/E/Y/F, V274I, N302V/L/Y, N305V/L/Y, S306T/V, Q308K/R/A/S/T, Y309F, Y310E/D/Q/N/L/V/I, D314A/S/T, L409N, D408S/T, A410S/T, D413R/K/S/T, A415S/T, G416S/T/V, 10 N418A/V/S/T, S419D/N/T, K421E/Q/S/T/V/A, H422D/L/Y/F, I423L/V/S/T/N/Q, T424S/A and K426A/S/T.

Other substitutions which are considered of particular importance in SEQ ID NO:3 include D437N and D440N.

Similar modifications, e.g. substitutions, may be introduced in equivalent positions of 15 other pullulanases. Modifications of particular interest are any combination of one or more of the above with any of the other modifications disclosed herein.

Before actually constructing a pullulanase variant to achieve any of the above objectives, it may be convenient to evaluate whether or not the contemplated amino acid modification can be accommodated into pullulanase structure, e.g. in a model of 20 the three-dimensional structure of the parent pullulanase.

### **Pullulanase variants with an altered substrate specificity**

One aim of the present invention is to change the degradation characteristics of a pullulanase. Thus, as Promozyme® (and pullulanases in general) exhibits a low activity towards high molecular weight branched starchy material, such as glycogen and 25 amylopectin, it may be desirable to change this cleavage pattern, e.g. so as to obtain a

higher activity against such substrates, in particular when the pullulanase is to be added during the liquefaction process.

An altered substrate specificity may be achieved by modifying the substrate binding area in a parent pullulanase.

5 Accordingly, the present invention also relates to a method for constructing a variant of a parent pullulanase, the method comprising:

a) identifying the substrate binding area in a model of the three-dimensional structure of the parent pullulanase;

10 b) modifying the substrate binding area by an amino acid substitution, deletion and/or insertion;

c) optionally repeating step b) recursively;

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b),

e) preparing the variant resulting from steps a) - d);

15 f) testing the substrate specificity of the variant;

g) optionally repeating steps a) - f) recursively; and

h) selecting a variant having an altered substrate specificity as compared to the parent pullulanase.

The substrate binding area may easily be identified by homology to other family 13  
20 members. The active site residues are identified by homology. The substrate-binding site is identified by the concave cavity containing the active site residues. A substrate model is docked into the cavity. A suitable substrate model is the substrate structure found in the pdb file 1BAG termed GLC. This model can be "docked" into the Promozyme X-ray structure or a modeled Pullulanase 3D structure by superimposing  
25 the active site residues in the two structures. In 1BAG one of the active site residues

has been mutated into an Gln instead of the native Glu. The active site residues to be superimposed are: D269, Q208 and D176 (1BAG) with D736, E651 and D622 (Promozyme®). The superposition can be made using the program INSIGHTII.

Without being limited to any theory, it is presently believed that binding between a  
5 substrate and an enzyme is supported by favorable interactions found within a sphere  
10 10 Å from the substrate molecule, in particular within a sphere of 6 Å from the substrate  
molecule. Examples of such favorable bonds are hydrogen bonds, strong electrostatic  
interaction and/or hydrophobic interactions. The following residues of Promozyme®  
(SEQ ID NO: 1), are within a distance of 10 Å from the “docked” substrate and thus  
believed to be involved in interactions with said substrate:

437, 439, 487, 489, 490, 514, 679, 681, 684, 685, 731, 775, 786,

494-496 (i.e. 494, 495 and 496),

505-511 (i.e. 505, 506, 507, 508, 509, 510 and 511),

551-559 (i.e. 551, 552, 553, 554, 555, 556, 557, 558 and 559),

15 584-590 (i.e. 584, 585, 586, 587, 588, 589 and 590),

620-626 (i.e. 620, 621, 622, 623, 624, 625, 626),

650-658 (i.e. 659, 651, 652, 653, 654, 655, 656, 657 and 568),

665-668 (i.e. 666, 667 and 668),

690-693 (i.e. 690, 691, 692 and 693),

20 734-738 (i.e. 734, 735, 736, 737 and 738) and

789-795 (i.e. 789, 790, 791, 792, 793, 794 and 795).

The following residues of Promozyme® are within a distance of 6 Å from the substrate  
and thus believed to be involved in interactions with said substrate:

489, 551, 553, 555, 556, 620, 651, 691, 692, 791, 793, 794,

506-510 (i.e. 507, 508, 509 and 510),

586-588 (i.e. 586, 587 and 588),

622-624 (i.e. 622, 623 and 624),

5 653-656 (i.e. 653, 654, 655 and 656) and

735-737 (i.e. 735, 736 and 737),

In a preferred embodiment of the invention, the parent pullulanase is modified in such a way that the variant pullulanase exhibits an increased isoamylase activity compared to the parent pullulanase.

- 10 When used herein, the term “increased isoamylase activity” refers in general to the fact that the pullulanase variants according to the invention exhibits a higher activity towards high molecular weight branched starchy material, such as glycogen and amylopectin as compared to the parent pullulanase, cf. above.

- 15 In an interesting embodiment of the invention the pullulanase variant has an increased isoamylase activity as defined by an increase of at least 5%, preferably of at least 10%, more preferably of at least 15%, more preferably of at least 25%, most preferably of at least 50%, in particular of at least 75%, such as of at least 100% in the number of reducing ends formed in the “assay for isoamylase-like activity” described herein, using 50 mM sodium acetate, a pH of 4.5, 5.0 or 5.5, a temperature of 60°C and when
- 20 incubated with a 10 w/v rabbit liver glycogen solution for a period of 10 min.

Similar modifications may be introduced in equivalent positions of other pullulanases. Substitutions of particular interest are any combination of one or both of the above with any of the other modifications disclosed herein.



For example, the following residues of the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) are within a distance of 10 Å from the “docked” substrate and thus believed to be involved in interactions with said substrate:

435, 437, 485, 487, 488, 512, 677, 679, 682, 683, 729, 773, 784,

5

492-494 (i.e. 492, 493 and 494),

503-509 (i.e. 503, 504, 505, 506, 507, 508 and 509),

10 549-557 (i.e. 549, 550, 551, 552, 553, 554, 555, 556 and 557),

582-588 (i.e. 582, 583, 584, 585, 586, 587 and 588),

618-624 (i.e. 618, 619, 620, 621, 622, 623 and 624),

15

648-656 (648, 649, 650, 651, 652, 653, 654, 655 and 656),

663-666 (i.e. 663, 664, 665 and 666),

20 688-691 (i.e. 688, 689, 690 and 691),

732-736 (732, 733, 734, 735 and 736) and

787-793 (i.e. 787, 788, 879, 790, 791, 792 and 793).

25 The following residues of the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) are within a distance of 6 Å from the substrate and thus believed to be involved in interactions with said substrate:

487, 549, 551, 553, 554, 618, 649, 689, 690, 789, 791, 792,

30 504-508 (i.e. 504, 505, 506, 507 and 508),

584-586 (i.e. 584, 585 and 586),

620-622 (i.e. 620, 621 and 622),

5

651-654 (i.e. 651, 652, 653 and 654) and

733-735 (i.e. 733, 734 and 735).

- 10 Examples of specific modifications in the above-mentioned regions of *Bacillus deramificans* are: L621I/V, D508M/N/L/T/V, T586I/L/V, T677W/F/Y, Y729F/I/L, D679G/A/V, S732V/T/L/I, N735G/L/V/I/S/T/A and  $\Delta$ (688-691).

#### **Pullulanase variants with altered pH dependent activity profile**

- 15 The pH dependent activity profile can be changed by changing the pKa of residues within 15 Å, in particular by changing the pKa of residues within 10 Å, from the active site residues of the parent pullulanase. Changing the pKa of the active site residues is achieved, e.g., by changing the electrostatic interaction or hydrophobic interaction between functional groups of amino acid side chains of a given amino acid residue and
- 20 its close surroundings. To obtain a higher activity at a higher pH, negatively charged residues are placed near a hydrogen donor acid, whereas positively charged residues placed near a nucleophilic acid will result in higher activity at low pH. Also, a decrease in the pKa can be obtained by reducing the accessibility of water or increasing hydrophobicity of the environment.
- 25 It is preferred that the variant in question exhibits a pH optimum which is at least about 0.5 pH units higher or lower, preferably at least about 1.0 pH units higher or lower, than the corresponding pH optimum of the parent pullulanase when tested on a suitable substrate (e.g. pullulan, amylopectin or glycogen).

Furthermore, it is particular preferred that the variant in question exhibits an increased activity in the pH range of from 4 to 5.5 as compared to the parent pullulanase when tested on a suitable substrate (e.g. pullulan, amylopectin or glycogen).

Thus, another aspect of the present invention relates to a method for constructing a  
5 variant of a parent pullulanase, the method comprising:

- a) identifying an amino acid residue which is within 15 Å, in particular within 10 Å, from an active site residue of the parent pullulanase in the three-dimensional structure of said parent pullulanase, and which is involved in electrostatic or hydrophobic interactions with an active site residue;
- 10 b) substituting said amino acid residue with another amino acid residue which changes the electrostatic and/or hydrophobic surroundings of an active site residue, and which can be accommodated in the structure;
- c) optionally repeating steps a) and b) recursively;
- d) optionally, making alterations each of which is an insertion, a deletion or a  
15 substitution of an amino acid residue at one or more positions other than b);
- e) preparing the variant resulting from steps a) - d);
- f) testing the pH dependent activity of said variant; and
- g) optionally repeating steps a) - f) recursively; and
- h) selecting a variant having an altered pH dependent activity as compared to the  
20 parent amylose.

In general, an amino acid residue which is within 15 Å or 10 Å, respectively, from an active site residue of the parent pullulanase may be identified by using the INSIGHTII program.

In a preferred embodiment, the variant of a parent pullulanase having an altered pH  
25 dependent activity profile as compared to the parent pullulanase comprises a

modification, e.g. a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1 (all within 15Å from the active site residues D736, E651, D622):

430, 433, 518, 521, 565, 599, 600, 610, 611, 635, 636, 639, 717, 760, 763, 764, 767,  
5 817,

435-443 (i.e. 435, 436, 437, 438, 439, 440, 441, 442, and 443),

486-496 (i.e. 486, 487, 488, 489, 490, 491, 492, 493, 494, 495 and 496),

505-515 (i.e. 505, 506, 507, 508, 509, 510, 511, 512, 513, 514 and 515),

548-560 (i.e. 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559 and 560),

10 573-575, (i.e. 573, 574 and 575),

583-595 (i.e. 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594 and 594),

602-604 (i.e. 602, 603 and 604),

606-608 (i.e. 606-607 and 608),

616-633 (i.e. 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629,  
15 630, 631, 632, and 633),

646-672 (i.e. 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659,  
660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671 and 672),

674-696 (i.e. 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687,  
688, 689, 690, 691, 692, 693, 694, 695 and 696),

20 720-722 (i.e. 720, 721 and 722),

725-747 (i.e. 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738,  
739, 740, 741, 742, 743, 744, 745, 746 and 747),

773-781 (i.e. 773, 774, 775, 776, 777, 778, 779, 780 and 781),

783-797 (i.e. 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796 and 797) and

799-802 (i.e. 799, 800, 801 and 802).

5 Within 10Å from the active site residues D736, E651, D622:

437, 442, 492, 514, 575, 594, 603, 632, 635, 684, 688, 691, 692, 721, 727, 729, 742, 743, 775, 777, 778, 780, 784, 786, 800,

487-490 (i.e. 487, 488, 489 and 490),

507-511 (i.e. 507, 508, 509, 510 and 511),

10 550-557 (i.e. 550, 551, 552, 553, 554, 555, 556 and 556),

585-588 (i.e. 585, 586, 587 and 588),

590-592 (i.e. 590, 591 and 592),

619-628 (i.e. 619, 620, 621, 622, 623, 624, 625, 626, 627 and 628),

648-655 (i.e. 648, 649, 650, 651, 652, 653, 654 and 655),

15 665-671 (i.e. 665, 666, 667, 668, 669, 670 and 671),

676-681 (i.e. 676, 677, 678, 679, 680 and 681),

731-740 (i.e. 731, 732, 733, 734, 735, 736, 737, 738, 739 and 740) and

788-793 (i.e. 788, 789, 790, 791, 792 and 793).

Similar modifications may be introduced in equivalent positions of other pullulanases.

20 Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

Thus, in another preferred embodiment, the variant of a parent pullulanase having an altered pH dependent activity profile as compared to the parent pullulanase comprises a modification, e.g. a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 3  
5 (all within 15 Å from the active site residues D734, E649 and D620):

428, 431, 516, 519, 563, 597, 598, 608, 609, 633, 634, 637, 715, 758, 761, 762, 765,  
815,

10 433-441 (i.e. 433, 434, 435, 436, 437, 438, 439, 440 and 441),

484-494 (i.e. 484, 485, 486, 487, 488, 489, 490, 491, 492, 493 and 494),

503-513 (i.e. 503, 504, 505, 506, 507, 508, 509, 510, 511, 512 and 513),

15

546-558 (546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557 and 558),

571-573 (i.e. 571, 572 and 573),

20 581-593 (i.e. 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592 and 593),

600-602 (i.e. 600, 601 and 602),

604-606 (i.e. 604, 605 and 606),

25

614-631 (i.e. 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627,  
628, 629, 630 and 631),

644-670 (i.e. 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657,

30 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669 and 670),

672-694 (i.e. 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693 and 694),

718-720 (i.e. 718, 719 and 720),

5

723-745 (i.e. 723, 734, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744 and 745),

771-779 (i.e. 771, 772, 773, 774, 775, 776, 777, 778 and 779),

10

781-795 (i.e. 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794 and 795) and

797-800 (i.e. 797, 798, 799 and 800).

15

Within 10 Å from the active site residues D734, E649 and D620:

435, 440, 490, 512, 573, 601, 605, 630, 669, 682, 686, 689, 690, 719, 725, 727, 740, 741, 773, 775, 776, 778, 782, 784, 798,

485-488 (i.e. 485, 486, 487 and 488),

20 505-509 (i.e. 505, 506, 507, 508 and 509),

548-555 (i.e. 548, 549, 550, 551, 552, 553, 554 and 555),

583-586 (i.e. 583, 584, 585 and 586),

588-590 (i.e. 588, 589 and 590),

617-626 (i.e. 616, 617, 618, 619, 620, 621, 622, 623, 624, 625 and 626),

25 646-653 (i.e. 646, 647, 648, 649, 650, 651, 652 and 653),

663-667 (i.e. 663, 664, 665, 666 and 667),

674-679 (i.e. 674, 675, 676, 677, 678 and 679),

729-738 (i.e. 729, 730, 731, 732, 733, 734, 735, 736, 737 and 738) and

786-791 (i.e. 786, 787, 788, 789, 790 and 791).

Specific examples of substitutions in the above-mentioned positions include  
5 D437L/I/V/F, D440L/I/V/F, M486K, M487K, D503L/I/V/F, D508N/L/T/V, T586V/I,  
M630H and D437L/I/V/F+D440L/I/V/F+D503L/I/V/F.

### **Nomenclature for amino acid modifications**

The nomenclature used herein for defining modifications is essentially as described in  
WO 92/05249. Thus, G406A indicates a substitution of the amino acid G (Gly) in  
10 position 406 with the amino acid A (Ala). G406 indicates a substitution of the amino acid  
G (Gly) with any other amino acid. P394F/W/I/L indicates a substitution of P394 with F,  
W, I or L. Δ(688-691) indicates a deletion of amino acids in positions 688-691. 412-A-  
413 indicates an insertion of A between amino acids 412 and 413.

When used herein, the term "modification" (of a particular amino acid residue) is  
15 intended to cover substitution and deletion (of the particular amino acid residue) as well  
as insertion of one or more amino acid residues after the particular amino acid residue.

### **Polypeptide sequence homology**

For purposes of the present invention, the degree of homology may be suitably  
determined according to the method described in S.B. Needleman and C.D. Wunsch,  
20 *Journal of Molecular Biology*, **48**, 443-45, with the following settings for polypeptide  
sequence comparison: GAP creation penalty of 3.0 and GAP extension penalty of 0.1.  
The determination may be done by means of a computer program known such as GAP  
provided in the UWGCG program package (Program Manual for the Wisconsin  
Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive,  
25 Madison, Wisconsin, USA 53711).

### **Hybridization**



Suitable experimental conditions for determining hybridization between a nucleotide probe and a homologous DNA or RNA sequence involves presoaking of the filter containing the DNA fragments or RNA to hybridize in 5x SSC (sodium chloride/sodium citrate, Sambrook, et al. Molecular Cloning: A Laboratory Manual, 2<sup>nd</sup> Ed., Cold Spring Harbor, 1989) for 10 min, and prehybridization of the filter in a solution of 5x SSC, 5x Denhardt's solution (Sambrook, et al., 1989), 0.5% SDS and 100 µg/ml of denatured sonicated salmon sperm DNA (Sambrook, et al., 1989), followed by hybridization in the same solution containing a random-primed (A. P. Feinberg B. and Vogelstein, *Anal. Biochem.* **132**, 6-13 (1983)), <sup>32</sup>P-dCTP-labeled (specific activity > 1 x 10<sup>9</sup> cpm/µg ) probe for 12 hours at ca. 45°C. The filter is then washed twice for 30 minutes in 2x SSC, 0.5% SDS at least 55°C (low stringency), preferably at least 60°C (medium stringency), more preferably at least 65°C (medium/high stringency), more preferably at least 70°C (high stringency), even more preferably at least 75°C (very high stringency).

Molecules which hybridize to the oligonucleotide probe under these conditions are detected by exposure to x-ray film.

### **Methods of preparing pullulanase variants according to the invention**

#### **Cloning a DNA sequence encoding a pullulanase**

The DNA sequence encoding a parent pullulanase may be isolated from any cell or microorganism producing the pullulanase in question, using various methods well known in the art.

First, a genomic DNA and/or cDNA library should be constructed using chromosomal DNA or messenger RNA from the organism that produces the pullulanase to be studied. Then, if the amino acid sequence of the pullulanase is known, homologous, labelled oligonucleotide probes may be synthesised and used to identify pullulanase-encoding clones from a genomic library prepared from the organism in question. Alternatively, a labelled oligonucleotide probe containing sequences homologous to a known pullulanase gene could be used as a probe to identify pullulanase-encoding clones, using hybridization and washing conditions of lower stringency.

Alternatively, the DNA sequence encoding the enzyme may be prepared synthetically by established standard methods, e.g. the phosphoroamidite method described by S.L. Beaucage and M.H. Caruthers, *Tetrahedron Letters*, **22**, 1859-1869 (1981) or the method described by Matthes et al. *The EMBO*, **3**, 801-805 (1984). In the phosphoroamidite method, oligonucleotides are synthesized, e.g. in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors.

Finally, the DNA sequence may be of mixed genomic and synthetic origin, mixed synthetic and cDNA origin or mixed genomic and cDNA origin, prepared by ligating fragments of synthetic, genomic or cDNA origin, wherein the fragments correspond to various parts of the entire DNA sequence, in accordance with techniques well known in the art. The DNA sequence may also be prepared by polymerase chain reaction (PCR) using specific primers, for instance as described in US 4,683,202 or R.K. Saiki et al. *Science*, **239**, 487-491(1988).

#### Site-directed Mutagenesis

Once a pullulanase-encoding DNA sequence has been isolated, and desirable sites for modification identified, modifications may be introduced using synthetic oligonucleotides. These oligonucleotides contain nucleotide sequences flanking the desired modification sites; mutant nucleotides are inserted during oligonucleotide synthesis. In a specific method, a single-stranded gap of DNA, bridging the pullulanase-encoding sequence, is created in a vector carrying the pullulanase gene. Then the synthetic nucleotide, bearing the desired modification, is annealed to a homologous portion of the single-stranded DNA. The remaining gap is then filled in with DNA polymerase I (Klenow fragment) and the construct is ligated using T4 ligase. A specific example of this method is described in Morinaga et al. *Biotechnology* **2**, 639-646 (1984). US 4,760,025 discloses the introduction of oligonucleotides encoding multiple modifications by performing minor alterations of the cassette. However, an even greater variety of modifications can be introduced at any one time by the Morinaga method because a multitude of oligonucleotides, of various lengths, can be introduced.

Another method of introducing modifications into a pullulanase-encoding DNA sequences is described in Nelson and Long *Analytical Biochemistry*, **180**, 147-151 (1989). It involves a 3-step generation of a PCR fragment containing the desired modification introduced by using a chemically synthesized DNA strand as one of the  
5 primers in the PCR reactions. From the PCR-generated fragment, a DNA fragment carrying the modification may be isolated by cleavage with restriction endonucleases and reinserted into an expression plasmid.

### Random Mutagenesis

Random mutagenesis is suitably performed either as localized or region-specific  
10 random mutagenesis in at least three parts of the gene translating to the amino acid sequence shown in question, or within the whole gene.

The random mutagenesis of a DNA sequence encoding a parent pullulanase may be conveniently performed by use of any method known in the art.

In relation to the above, a further aspect of the present invention relates to a method for  
15 generating a variant of a parent pullulanase, wherein the variant exhibits an altered property, such as increased thermostability, increased stability at low pH and at low calcium concentration, relative to the parent pullulanase, the method comprising:

- (a) subjecting a DNA sequence encoding the parent pullulanase to random mutagenesis,
- 20 (b) expressing the mutated DNA sequence obtained in step (a) in a host cell, and
- (c) screening for host cells expressing a pullulanase variant which has an altered property relative to the parent pullulanase.

Step (a) of the above method of the invention is preferably performed using doped primers.

25 For instance, the random mutagenesis may be performed by use of a suitable physical or chemical mutagenizing agent, by use of a suitable oligonucleotide, or by subjecting

the DNA sequence to PCR generated mutagenesis. Furthermore, the random mutagenesis may be performed by use of any combination of these mutagenizing agents. The mutagenizing agent may, e.g., be one which induces transitions, transversions, inversions, scrambling, deletions, and/or insertions.

- 5 Examples of a physical or chemical mutagenizing agent suitable for the present purpose include ultraviolet (UV) irradiation, hydroxylamine, N-methyl-N'-nitro-N-nitrosoguanidine (MNNG), O-methyl hydroxylamine, nitrous acid, ethyl methane sulphonate (EMS), sodium bisulphite, formic acid, and nucleotide analogues. When such agents are used, the mutagenesis is typically performed by incubating the DNA  
10 sequence encoding the parent enzyme to be mutagenized in the presence of the mutagenizing agent of choice under suitable conditions for the mutagenesis to take place, and selecting for mutated DNA having the desired properties.

When the mutagenesis is performed by the use of an oligonucleotide, the oligonucleotide may be doped or spiked with the three non-parent nucleotides during  
15 the synthesis of the oligonucleotide at the positions which are to be changed. The doping or spiking may be done so that codons for unwanted amino acids are avoided. The doped or spiked oligonucleotide can be incorporated into the DNA encoding the pullulaase enzyme by any published technique, using e.g. PCR, LCR or any DNA polymerase and ligase as deemed appropriate.

- 20 Preferably, the doping is carried out using "constant random doping", in which the percentage of wild-type and modification in each position is predefined. Furthermore, the doping may be directed toward a preference for the introduction of certain nucleotides, and thereby a preference for the introduction of one or more specific amino acid residues. The doping may be made, e.g., so as to allow for the introduction of 90%  
25 wild type and 10% modifications in each position. An additional consideration in the choice of a doping scheme is based on genetic as well as protein-structural constraints. The doping scheme may be made by using the DOPE program which, *inter alia*, ensures that introduction of stop codons is avoided (L.J. Jensen et al. *Nucleic Acid Research*, **26**, 697-702 (1998)).

When PCR-generated mutagenesis is used, either a chemically treated or non-treated gene encoding a parent pullulanase enzyme is subjected to PCR under conditions that increase the misincorporation of nucleotides (Deshler 1992; Leung et al., *Technique*, 1, 1989, pp. 11-15).

- 5 A mutator strain of *E. coli* (Fowler et al., *Molec. Gen. Genet.*, **133**, 1974, 179-191), *S. cerevisiae* or any other microbial organism may be used for the random mutagenesis of the DNA encoding the pullulanase by, e.g., transforming a plasmid containing the parent enzyme into the mutator strain, growing the mutator strain with the plasmid and isolating the mutated plasmid from the mutator strain. The mutated plasmid may be
- 10 subsequently transformed into the expression organism.

The DNA sequence to be mutagenized may conveniently be present in a genomic or cDNA library prepared from an organism expressing the parent pullulanase. Alternatively, the DNA sequence may be present on a suitable vector such as a plasmid or a bacteriophage, which as such may be incubated with or otherwise exposed to the

15 mutagenising agent. The DNA to be mutagenized may also be present in a host cell either by being integrated in the genome of said cell or by being present on a vector harbored in the cell. Finally, the DNA to be mutagenized may be in isolated form. It will be understood that the DNA sequence to be subjected to random mutagenesis is preferably a cDNA or a genomic DNA sequence.

- 20 In some cases it may be convenient to amplify the mutated DNA sequence prior to performing the expression step b) or the screening step c). Such amplification may be performed in accordance with methods known in the art, the presently preferred method being PCR-generated amplification using oligonucleotide primers prepared on the basis of the DNA or amino acid sequence of the parent enzyme.

- 25 Subsequent to the incubation with or exposure to the mutagenising agent, the mutated DNA is expressed by culturing a suitable host cell carrying the DNA sequence under conditions allowing expression to take place. The host cell used for this purpose may be one which has been transformed with the mutated DNA sequence, optionally present on a vector, or one which was carried the DNA sequence encoding the parent enzyme

during the mutagenesis treatment. Examples of suitable host cells are the following:  
gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*,  
*Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus*  
*amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus*  
5 *megaterium*, *Bacillus thuringiensis*, *Streptomyces lividans* or *Streptomyces murinus*;  
and gram negative bacteria such as *E. coli*.

The mutated DNA sequence may further comprise a DNA sequence encoding functions  
permitting expression of the mutated DNA sequence.

#### Localized random mutagenesis

- 10 The random mutagenesis may be advantageously localized to a part of the parent  
pullulanase in question. This may, e.g., be advantageous when certain regions of the  
enzyme have been identified to be of particular importance for a given property of the  
enzyme, and when modified are expected to result in a variant having improved  
properties. Such regions may normally be identified when the tertiary structure of the  
15 parent enzyme has been elucidated and related to the function of the enzyme.

The localized, or region-specific, random mutagenesis is conveniently performed by use  
of PCR generated mutagenesis techniques as described above or any other suitable  
technique known in the art. Alternatively, the DNA sequence encoding the part of the  
DNA sequence to be modified may be isolated, e.g., by insertion into a suitable vector,  
20 and said part may be subsequently subjected to mutagenesis by use of any of the  
mutagenesis methods discussed above.

#### General method for random mutagenesis by use of the DOPE program

The random mutagenesis may be carried out by the following steps:

1. Select regions of interest for modification in the parent enzyme
- 25 2. Decide on mutation sites and non-mutated sites in the selected region

3. Decide on which kind of mutations should be carried out, e.g. with respect to the desired stability and/or performance of the variant to be constructed
  4. Select structurally reasonable mutations
  5. Adjust the residues selected by step 3 with regard to step 4.
  - 5 6. Analyze by use of a suitable dope algorithm the nucleotide distribution.
  7. If necessary, adjust the wanted residues to genetic code realism, e.g. taking into account constraints resulting from the genetic code, e.g. in order to avoid introduction of stop codons; the skilled person will be aware that some codon combinations cannot be used in practice and will need to be adapted
  - 10 8. Make primers
  9. Perform random mutagenesis by use of the primers
  10. Select resulting pullulanase variants by screening for the desired improved properties.
- Suitable dope algorithms for use in step 6 are well known in the art. One such algorithm is described by Tomandl, D. et al., 1997, Journal of Computer-Aided Molecular Design 11:29-38. Another algorithm is DOPE (Jensen, LJ, Andersen, KV, Svendsen, A, and Kretzschmar, T (1998) Nucleic Acids Research 26:697-702).

#### Expression of pullulanase variants

The construction of the variant of interest is accomplished by cultivating a microorganism comprising a DNA sequence encoding the variant under conditions which are conducive for producing the variant, and optionally subsequently recovering the variant from the resulting culture broth. This is described in detail further below.

According to the invention, a DNA sequence encoding the variant produced by methods described above, or by any alternative methods known in the art, can be expressed, in the form of a protein or polypeptide, using an expression vector which typically includes

control sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

The recombinant expression vector carrying the DNA sequence encoding an pullulanase variant of the invention may be any vector which may conveniently be  
5 subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e. a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g. a plasmid, a bacteriophage or an extrachromosomal element, minichromosome or an  
10 artificial chromosome. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

In the vector, the DNA sequence should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional  
15 activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of the DNA sequence encoding a pullulanase variant of the invention, especially in a bacterial host, are the promoter of the *lac* operon of *E.coli*, the *Streptomyces coelicolor* agarase gene *dagA* promoters, the promoters of the *Bacillus li-*  
20 *cheniformis*  $\alpha$ -amylase gene (*amyL*), the promoters of the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the promoters of the *Bacillus amyloliquefaciens*  $\alpha$ -amylase (*amyQ*), the promoters of the *Bacillus subtilis* *xylA* and *xylB* genes, etc. For transcription in a fungal host, examples of useful promoters are those derived from the gene encoding *A. oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *A.*  
25 *niger* neutral  $\alpha$ -amylase, *A. niger* acid stable  $\alpha$ -amylase, *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase or *A. nidulans* acetamidase.

The expression vector of the invention may also comprise a suitable transcription terminator and, in eukaryotes, polyadenylation sequences operably connected to the



DNA sequence encoding the pullulanase variant of the invention. Termination and polyadenylation sequences may suitably be derived from the same sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. Examples of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the *dal* genes from *B. subtilis* or *B. licheniformis*, or one which confers antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracycline resistance. Furthermore, the vector may comprise *Aspergillus* selection markers such as *amdS*, *argB*, *niaD* and *sC*, a marker giving rise to hygromycin resistance, or the selection may be accomplished by co-transformation, e.g. as described in WO 91/17243.

While intracellular expression may be advantageous in some respects, e.g. when using certain bacteria as host cells, it is generally preferred that the expression is extracellular. In general, the *Bacillus*  $\alpha$ -amylases mentioned herein comprise a preregion permitting secretion of the expressed protease into the culture medium. If desirable, this preregion may be replaced by a different preregion or signal sequence, conveniently accomplished by substitution of the DNA sequences encoding the respective preregions.

The procedures used to ligate the DNA construct of the invention encoding the pullulanase variant, the promoter, terminator and other elements, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance, Sambrook et al. Molecular Cloning: A Laboratory Manual, 2<sup>nd</sup> Ed., Cold Spring Harbor, 1989).

The cell of the invention, either comprising a DNA construct or an expression vector of the invention as defined above, is advantageously used as a host cell in the recombinant production of a pullulanase variant of the invention. The cell may be

transformed with the DNA construct of the invention encoding the variant, conveniently by integrating the DNA construct (in one or more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of the DNA constructs into the host  
5 chromosome may be performed according to conventional methods, e.g. by homologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an  
10 insect, but is preferably a microbial cell, e.g. a bacterial or a fungal (including yeast) cell.

Examples of suitable bacteria are gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*,  
15 *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, or *Streptomyces lividans* or *Streptomyces murinus*, or gram negative bacteria such as *E.coli*. The transformation of the bacteria may, for instance, be effected by protoplast transformation or by using competent cells in a manner known *per se*.

The yeast organism may favourably be selected from a species of *Saccharomyces* or  
20 *Schizosaccharomyces*, e.g. *Saccharomyces cerevisiae*. The filamentous fungus may advantageously belong to a species of *Aspergillus*, e.g. *Aspergillus oryzae* or *Aspergillus niger*. Fungal cells may be transformed by a process involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known *per se*. A suitable procedure for transformation of *Aspergillus* host cells  
25 is described in EP 238 023.

In a yet further aspect, the present invention relates to a method for producing a pullulanase variant of the invention, the method comprising: cultivating a host cell as described above under conditions conducive to the production of the variant and recovering the variant from the cells and/or culture medium.

The medium used to cultivate the cells may be any conventional medium suitable for growing the host cell in question and obtaining expression of the pullulanase variant of the invention. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g. as described in catalogues of the  
5 American Type Culture Collection).

The pullulanase variant secreted from the host cells may conveniently be recovered from the culture medium by well-known procedures, including separating the cells from the medium by centrifugation or filtration, and precipitating proteinaceous components of the medium by means of a salt such as ammonium sulfate, followed by the use of  
10 chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

### **Testing of pullulanase**

Pullulanase variants produced by any of the methods described above may be tested, either prior to or after purification, for pullulanase activity in a screening assay which  
15 measures the ability of the variant to degrade pullulan or, in case it is desired to screen for an increased isoamylases activity, the ability of the variant to degrade amylopectin. The screening in step 10 in the above-mentioned random mutagenesis method of the invention may be conveniently performed by use of a filter assay based on the following procedure: A microorganism capable of expressing the mutated pullulanase of interest  
20 is incubated on a suitable medium and under suitable conditions for secretion of the enzyme, the medium being covered with two filters comprising a protein-binding filter placed under a second filter exhibiting a low protein binding capability. The microorganism is grown on the second, top filter. Subsequent to the incubation, the bottom protein-binding filter comprising enzymes secreted from the microorganism is  
25 separated from the second filter comprising the microorganism. The protein-binding filter is then subjected to screening for the desired enzymatic activity, and the corresponding microbial colonies present on the second filter are identified. The first filter used for binding the enzymatic activity may be any protein-binding filter, e.g., nylon or nitrocellulose. The second filter carrying the colonies of the expression organism may

be any filter that has no or low affinity for binding proteins, e.g., cellulose acetate or Durapore™.

Screening consists of treating the first filter to which the secreted protein is bound with a substrate that allows detection of the activity. The enzymatic activity may be detected  
5 by a dye, fluorescence, precipitation, pH indicator, IR-absorbance or any other known technique for detection of enzymatic activity. The detecting compound may be immobilized by any immobilizing agent e.g. agarose, agar, gelatine, polyacrylamide, starch, filter paper, cloth; or any combination of immobilizing agents. For example, isoamylase activity can be detected by Cibacron Red labelled amylopectin, which is  
10 immobilized in agarose. isoamylase activity on this substrate produces zones on the plate with reduced red color intensity (clearing zones).

To screen for variants with increased stability, the filter with bound pullulanase variants can be pretreated prior to the detection step described above to inactivate variants that do not have improved stability relative to the parent pullulanase. This inactivation step  
15 may consist of, but is not limited to, incubation at elevated temperatures in the presence of a buffered solution at any pH from pH 2 to 12, and/or in a buffer containing another compound known or thought to contribute to altered stability e.g., surfactants, EDTA, EGTA, wheat flour components, or any other relevant additives. Filters so treated for a specified time are then rinsed briefly in deionized water and placed on  
20 plates for activity detection as described above. The conditions are chosen such that stabilized variants show increased enzymatic activity relative to the parent after incubation on the detection media.

To screen for variants with altered thermostability, filters with bound variants are incubated in buffer at a given pH (e.g., in the range from pH 2-12) at an elevated  
25 temperature (e.g., in the range from 50°-110°C) for a time period (e.g., from 1-20 minutes) to inactivate nearly all of the parent pullulanase, rinsed in water, then placed directly on a detection plate containing immobilized Cibacron Blue labeled pullulan and incubated until activity is detectable. As will be understood, thermostability and increased isoamylase activity may be tested simultaneously by using a detection plate

containing immobilized Cibacron Red labeled amylopectin and incubate until activity is detectable. Moreover, pH dependent stability can be screened for by adjusting the pH of the buffer in the above inactivation step such that the parent pullulanase is inactivated, thereby allowing detection of only those variants with increased stability at the pH in question. To screen for variants with increased calcium-dependent stability, calcium chelators, such as ethylene glycol-bis( $\beta$ -aminoethyl ether) N,N,N',N'-tetraacetic acid (EGTA), is added to the inactivation buffer at a concentration such that the parent pullulanase is inactivated under conditions further defined, such as buffer pH, temperature or a specified length of incubation.

10 The variants of the invention may be suitably tested by assaying the pullulan- or amylopectin-degrading activity of the variant, for instance by growing host cells transformed with a DNA sequence encoding a variant on a starch-containing agarose plate and identifying pullulan- and/or amylopectin-degrading host cells as described above. Further testing in regard to altered properties, including specific activity, substrate  
15 specificity, cleavage pattern, thermoactivation, thermostability, pH dependent activity or optimum, pH dependent stability, temperature dependent activity or optimum, transglycosylation activity, stability, and any other parameter of interest, may be performed on purified variants in accordance with methods known in the art as described below.

20 The invention is further illustrated with reference to the following examples which are not intended to be in any way limiting to the scope of the invention as claimed.

## **EXAMPLES**

### **Determination of pullulanase activity**

Endo-pullulanase activity in NPUN is measured relative to a Novo Nordisk pullulanase  
25 standard. One pullulanase unit (NPUN) is defined as the amount of enzyme which releases 1 mmol glucose per minute under the standard conditions (0.7% red pullulan, pH 5, 40°C, 20 minutes). The activity is measured in NPUN/ml using red pullulan.

1 ml diluted sample or standard is incubated at 40°C for 2 minutes. 0.5 ml 2% red pullulan, 0.5 M KCl, 50 mM citric acid, pH 5 are added and mixed. The tubes are incubated at 40°C for 20 minutes and stopped by adding 2.5 ml 80% ethanol. The tubes are left standing at room temperature for 10-60 minutes followed by centrifugation  
5 10 minutes at 4000 rpm. OD of the supernatants is then measured at 510 nm and the activity calculated using a standard curve.

#### Expression of pullulanase from *Bacillus deramificans*

The pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) is expressed in *B. subtilis* from a plasmid denoted pCA36. This plasmid contains the complete gene encoding the  
10 pullulanase, the expression of which is directed by the promoter from *Bacillus amyloliquefaciens*  $\alpha$ -amylase. Further, the plasmid contains the origin of replication, *oriT*, from plasmid pUB110 and the *cat* gene from plasmid pC194 conferring resistance towards chloramphenicol. PCA36 is shown in Fig. 1.

#### Example 1: Construction of *Bacillus deramificans* D620A variant

15 Gene specific primer 132011 and mutagenic primer 132012 are used to amplify by PCR an approximately 410 bp DNA fragment from the pCA36 plasmid.

The 410 bp fragment is purified from an agarose gel and used as a Mega-primer together with primer 136054 in a second PCR carried out on the same template.

The resulting approximately 1110 bp fragment is digested with restriction enzymes  
20 BsiW I and Mlu I and the resulting approximately 330 bp DNA fragment is purified and ligated with the pCA36 plasmid digested with the same enzymes. Competent *Bacillus subtilis* SHA273 (amylase and protease low) cells are transformed with the ligation and chloramphenicol resistant transformants are checked by colony PCR.

The mutagenesis primer 132012 introduced the D620A substitution (written in bold in  
25 the primer seq.) and introduced simultaneously a Bgl I restriction site (underlined in the primer seq.), which facilitates easy pinpointing of mutants.

Finally, DNA sequencing was carried out to verify the presence of the correct mutations on the plasmid.

Primer 132011:

5' CGCTTCGGAATCATTAGGATTGC 3'

5 Primer 132012:

5' GCTTCCGTTTT**GCC**TTAATGGCGCTGC 3'

Primer 136054:

5' GGCCAAGGCTCTACCCGAACGGC 3'

Example 2: Construction of *Bacillus deramificans* E649A variant

- 10 This variant constructed as described in Example 1, except that mutagenic primer 132013 is used. The mutagenesis primer 132013 introduced the E649A substitution (written in bold in the primer seq.) and a Nar I restriction site(underlined in the primer seq.), which facilitates easy pinpointing of mutants.

Primer 132013:

- 15 5' GCACTTTACGGG**GCG**CCATGGACGGG 3'

APPENDIX 1

1	N	PRO A 112	80.159	5.264	-8.274	1.00 42.79	48	CE1	TYR A 118	73.073	-5.426	7.355	1.00 17.37
2	CA	PRO A 112	79.045	4.605	-7.604	1.00 41.43	49	CE2	TYR A 118	70.987	-4.499	6.586	1.00 17.81
3	C	PRO A 112	79.488	3.326	-6.903	1.00 39.90	50	CZ	TYR A 118	72.050	-4.480	7.470	1.00 17.70
4	O	PRO A 112	80.510	2.695	-7.236	1.00 39.13	51	OH	TYR A 118	72.116	-3.520	8.458	1.00 16.31
5	CB	PRO A 112	78.020	4.300	-8.676	1.00 41.58	52	N	LEU A 119	73.396	-10.483	4.417	1.00 17.54
6	CG	PRO A 112	78.845	4.164	-9.902	1.00 42.58	53	CA	LEU A 119	73.089	-11.871	4.133	1.00 17.55
7	CD	PRO A 112	79.947	5.166	-9.749	1.00 43.50	54	C	LEU A 119	71.822	-12.293	4.863	1.00 17.58
8	N	SER A 113	78.659	2.987	-5.901	1.00 36.72	55	O	LEU A 119	71.801	-12.501	6.070	1.00 16.85
9	CA	SER A 113	79.034	1.812	-5.120	1.00 35.45	56	CB	LEU A 119	74.257	-12.745	4.571	1.00 17.57
10	C	SER A 113	77.884	0.992	-4.544	1.00 33.99	57	CG	LEU A 119	74.043	-14.215	4.193	1.00 20.46
11	O	SER A 113	76.732	1.456	-4.501	1.00 33.34	58	CD1	LEU A 119	73.879	-14.416	2.682	1.00 20.82
12	CB	SER A 113	79.793	2.427	-3.932	1.00 36.77	59	CD2	LEU A 119	75.196	-15.116	4.624	1.00 21.33
13	CG	SER A 113	78.763	3.023	-3.107	1.00 37.94	60	N	ASP A 120	70.677	-12.315	4.183	1.00 17.72
14	N	VAL A 114	78.232	-0.222	-4.096	1.00 30.90	61	CA	ASP A 120	69.372	-12.510	4.811	1.00 16.35
15	CA	VAL A 114	77.141	-0.914	-3.375	1.00 31.03	62	C	ASP A 120	68.815	-13.933	4.760	1.00 17.71
16	C	VAL A 114	77.274	-0.292	-1.972	1.00 29.16	63	O	ASP A 120	67.794	-14.173	5.449	1.00 16.09
17	O	VAL A 114	78.389	-0.274	-1.420	1.00 31.09	64	CB	ASP A 120	68.314	-11.512	4.346	1.00 17.88
18	CB	VAL A 114	77.417	-2.419	-3.553	1.00 31.41	65	CG	ASP A 120	68.469	-10.114	4.912	1.00 18.37
19	CG1	VAL A 114	76.525	-3.253	-2.635	1.00 30.36	66	OD1	ASP A 120	69.040	-9.909	5.994	1.00 17.74
20	CG2	VAL A 114	77.488	-3.080	-4.917	1.00 30.56	67	OD2	ASP A 120	68.000	-9.132	4.295	1.00 21.04
21	N	SER A 115	76.266	0.401	-1.479	1.00 27.09	68	N	ASP A 121	69.459	-14.847	4.069	1.00 16.19
22	CA	SER A 115	76.390	1.084	-0.183	1.00 25.38	69	CA	ASP A 121	69.009	-16.253	4.082	1.00 19.25
23	C	SER A 115	76.091	0.149	0.997	1.00 24.90	70	C	ASP A 121	70.291	-17.036	3.749	1.00 18.78
24	O	SER A 115	76.347	0.637	2.117	1.00 24.00	71	O	ASP A 121	71.251	-16.347	3.404	1.00 16.73
25	CB	SER A 115	75.558	2.373	-0.187	1.00 22.77	72	CB	ASP A 121	67.838	-16.599	3.188	1.00 18.82
26	OG	SER A 115	74.201	2.001	-0.328	1.00 22.64	73	CG	ASP A 121	67.081	-17.860	3.551	1.00 21.17
27	N	ASN A 116	75.460	-0.989	0.840	1.00 23.19	74	OD1	ASP A 121	65.897	-17.937	3.106	1.00 21.16
28	CA	ASN A 116	75.223	-1.897	1.968	1.00 22.52	75	OD2	ASP A 121	67.552	-18.838	4.190	1.00 19.81
29	C	ASN A 116	74.830	-3.257	1.420	1.00 21.30	76	N	GLU A 122	70.312	-18.367	3.847	1.00 20.61
30	O	ASN A 116	74.230	-3.250	0.354	1.00 20.56	77	CA	GLU A 122	71.613	-19.020	3.562	1.00 23.88
31	CB	ASN A 116	74.117	-1.373	2.885	1.00 23.16	78	C	GLU A 122	72.181	-18.700	2.193	1.00 21.23
32	CG	ASN A 116	74.004	-2.136	4.191	1.00 21.84	79	O	GLU A 122	73.415	-18.680	2.060	1.00 20.25
33	OD1	ASN A 116	74.777	-1.866	5.122	1.00 20.82	80	CB	GLU A 122	71.517	-20.512	3.825	1.00 26.85
34	ND2	ASN A 116	73.090	-3.083	4.280	1.00 20.73	81	CG	GLU A 122	70.813	-21.249	2.697	1.00 31.98
35	N	ALA A 117	75.230	-4.313	2.098	1.00 19.74	82	CD	GLU A 122	70.644	-22.717	3.015	1.00 35.92
36	CA	ALA A 117	74.843	-5.672	1.740	1.00 19.18	83	OE1	GLU A 122	71.596	-23.371	3.499	1.00 38.33
37	C	ALA A 117	74.602	-6.504	3.002	1.00 20.75	84	OE2	GLU A 122	69.534	-23.235	2.779	1.00 40.26
38	O	ALA A 117	75.366	-6.467	3.957	1.00 21.21	85	N	LYS A 123	71.395	-18.480	1.147	1.00 21.26
39	CB	ALA A 117	75.831	-6.457	0.873	1.00 17.81	86	CA	LYS A 123	71.909	-18.121	-0.170	1.00 22.79
40	N	TYR A 118	73.479	-7.242	2.937	1.00 19.90	87	C	LYS A 123	71.247	-16.879	-0.755	1.00 22.17
41	CA	TYR A 118	73.080	-8.099	4.042	1.00 20.50	88	O	LYS A 123	71.137	-16.788	-1.992	1.00 22.07
42	C	TYR A 118	72.917	-9.549	3.578	1.00 19.96	89	CB	LYS A 123	71.655	-19.303	-1.115	1.00 24.69
43	O	TYR A 118	72.422	-9.839	2.494	1.00 22.33	90	CG	LYS A 123	72.497	-20.528	-0.798	1.00 27.82
44	CB	TYR A 118	71.739	-7.589	4.569	1.00 20.09	91	CD	LYS A 123	71.837	-21.782	-1.305	1.00 30.95
45	CG	TYR A 118	71.932	-6.424	5.476	1.00 18.77	92	CE	LYS A 123	72.745	-22.985	-1.438	1.00 33.61
							93	NZ	LYS A 123	71.885	-24.227	-1.408	1.00 38.51
							94	N	THR A 124	70.862	-15.914	0.062	1.00 18.31
							95	CA	THR A 124	70.223	-14.686	-0.397	1.00 19.05
							96	C	THR A 124	70.918	-13.424	0.117	1.00 19.03
							97	O	THR A 124	71.042	-13.313	1.342	1.00 18.19
							98	CB	THR A 124	68.759	-14.614	0.096	1.00 19.49
							99	OG1	THR A 124	68.093	-15.853	-0.273	1.00 21.02
							100	CG2	THR A 124	67.958	-13.436	-0.417	1.00 17.02
46	CD1	TYR A 118	73.008	-6.394	6.361	1.00 18.02							
47	CD2	TYR A 118	70.931	-5.460	5.586	1.00 17.79							



101	N	VAL A 125	71.314	-12.463	-0.717	1.00	18.66	154	C	PRO A 132	70.487	1.983	-11.172	1.00	39.15
102	CA	VAL A 125	71.852	-11.220	-0.221	1.00	20.11	155	O	PRO A 132	71.420	2.615	-11.696	1.00	39.25
103	C	VAL A 125	70.971	-10.047	-0.698	1.00	20.51	156	CB	PRO A 132	68.348	3.076	-10.341	1.00	39.31
104	O	VAL A 125	70.485	-10.031	-1.819	1.00	21.45	157	CG	PRO A 132	68.452	4.555	-10.271	1.00	39.22
105	CB	VAL A 125	73.343	-10.945	-0.302	1.00	22.08	158	CD	PRO A 132	69.703	4.916	-9.513	1.00	39.47
106	CG1	VAL A 125	74.227	-12.123	-0.759	1.00	21.11	159	N	MET A 133	70.115	0.773	-11.554	1.00	38.46
107	CG2	VAL A 125	73.756	-9.615	-0.901	1.00	19.94	160	CA	MET A 133	70.680	0.062	-12.683	1.00	37.37
108	N	LEU A 126	70.757	-9.068	-0.176	1.00	19.28	161	C	MET A 133	69.465	-0.615	-13.315	1.00	38.14
109	CA	LEU A 126	69.973	-7.883	-0.113	1.00	19.43	162	O	MET A 133	68.403	-0.628	-12.657	1.00	38.27
110	C	LEU A 126	70.940	-6.717	-0.189	1.00	20.40	163	CB	MET A 133	71.752	-0.962	-12.320	1.00	36.83
111	O	LEU A 126	71.583	-6.433	-0.840	1.00	17.65	164	CG	MET A 133	71.329	-2.070	-11.385	1.00	35.87
112	CB	LEU A 126	68.962	-7.679	1.033	1.00	19.40	165	SD	MET A 133	72.282	-3.590	-11.397	1.00	36.52
113	CG	LEU A 126	68.214	-6.352	0.939	1.00	21.05	166	CE	MET A 133	73.976	-3.108	-11.265	1.00	34.78
114	CD1	LEU A 126	67.147	-6.379	-0.146	1.00	17.96	167	N	THR A 134	69.598	-1.070	-14.564	1.00	38.11
115	CD2	LEU A 126	67.643	-5.843	2.254	1.00	18.86	168	CA	THR A 134	68.453	-1.786	-15.145	1.00	37.87
116	N	ALA A 127	71.204	-6.161	-1.360	1.00	20.21	169	C	THR A 134	69.034	-3.203	-15.229	1.00	38.03
117	CA	ALA A 127	72.232	-5.138	-1.506	1.00	23.09	170	O	THR A 134	70.166	-3.414	-15.885	1.00	35.72
118	C	ALA A 127	71.665	-3.800	-1.965	1.00	24.49	171	CB	THR A 134	67.747	-1.212	-16.362	1.00	39.56
119	O	ALA A 127	70.837	-3.785	-2.898	1.00	24.26	172	CG1	THR A 134	68.167	-1.836	-17.592	1.00	40.70
120	CB	ALA A 127	73.302	-5.630	-2.495	1.00	22.46	173	CG2	THR A 134	67.867	0.296	-16.567	1.00	38.10
121	N	LYS A 128	72.080	-2.709	-1.336	1.00	25.87	174	N	LEU A 135	68.277	-4.155	-14.682	1.00	38.56
122	CA	LYS A 128	71.568	-1.383	-1.764	1.00	27.63	175	CA	LEU A 135	68.779	-5.531	-14.645	1.00	38.93
123	C	LYS A 128	72.616	-0.764	-2.712	1.00	27.55	176	C	LEU A 135	68.807	-6.218	-16.003	1.00	40.69
124	O	LYS A 128	73.804	-0.895	-2.438	1.00	24.66	177	O	LEU A 135	67.927	-6.085	-16.837	1.00	40.85
125	CB	LYS A 128	71.296	-0.455	-0.592	1.00	26.80	178	CB	LEU A 135	67.967	-6.330	-13.628	1.00	36.13
126	CG	LYS A 128	70.839	0.946	0.922	1.00	27.35	179	CG	LEU A 135	67.915	-5.773	-12.197	1.00	33.81
127	CD	LYS A 128	69.376	1.128	-1.234	1.00	26.29	180	CD1	LEU A 135	66.758	-6.408	-11.456	1.00	33.44
128	CE	LYS A 128	69.084	2.556	-1.653	1.00	27.49	181	CD2	LEU A 135	69.218	-5.959	-11.427	1.00	31.63
129	NZ	LYS A 128	69.797	3.575	-0.866	1.00	29.77	182	N	ALA A 136	69.851	-7.010	-16.203	1.00	42.89
130	N	LEU A 129	72.178	-0.105	-3.777	1.00	29.12	183	CA	ALA A 136	69.985	-7.876	-17.381	1.00	43.50
131	CA	LEU A 129	73.115	0.531	-4.714	1.00	29.81	184	C	ALA A 136	69.636	-9.277	-16.895	1.00	44.87
132	C	LEU A 129	73.067	2.052	-4.625	1.00	30.79	185	O	ALA A 136	69.205	-9.395	-15.735	1.00	44.05
133	O	LEU A 129	71.997	2.621	-4.412	1.00	29.69	186	CB	ALA A 136	71.376	-7.739	-17.952	1.00	42.02
134	CB	LEU A 129	72.693	0.064	-6.092	1.00	29.38	187	N	ASP A 137	69.783	-10.304	-17.719	1.00	45.61
135	CG	LEU A 129	72.670	-1.425	-6.455	1.00	29.89	188	CA	ASP A 137	69.441	-11.652	-17.302	1.00	45.76
136	CD1	LEU A 129	72.293	-1.585	-7.931	1.00	30.38	189	C	ASP A 137	70.415	-12.326	-16.333	1.00	42.62
137	CD2	LEU A 129	74.009	-2.112	-6.236	1.00	28.39	190	O	ASP A 137	71.558	-11.918	-16.176	1.00	41.07
138	N	SER A 130	74.162	2.782	-4.801	1.00	32.54	191	CB	ASP A 137	69.547	-12.644	-18.479	1.00	49.36
139	CA	SER A 130	74.086	4.228	-4.641	1.00	34.33	192	CG	ASP A 137	68.263	-12.743	-19.277	1.00	52.75
140	C	SER A 130	73.299	4.884	-5.773	1.00	36.79	193	OD1	ASP A 137	68.067	-11.851	-20.128	1.00	54.23
141	O	SER A 130	73.009	6.074	-5.768	1.00	37.29	194	OD2	ASP A 137	67.474	-13.687	-19.039	1.00	54.86
142	CB	SER A 130	75.512	4.788	-4.600	1.00	33.55	195	N	ALA A 138	69.898	-13.417	-15.742	1.00	40.77
143	OG	SER A 130	76.227	4.352	-5.759	1.00	34.68	196	CA	ALA A 138	70.755	-14.138	-14.777	1.00	39.52
144	N	MET A 131	72.979	4.059	-6.795	1.00	37.15	197	C	ALA A 138	71.379	-13.240	-13.678	1.00	37.28
145	CA	MET A 131	72.225	4.581	-7.925	1.00	39.70	198	O	ALA A 138	70.708	-12.438	-13.041	1.00	35.69
146	C	MET A 131	71.602	3.473	-8.788	1.00	38.38	199	CB	ALA A 138	71.862	-14.845	-15.560	1.00	38.20
147	O	MET A 131	72.036	2.331	-8.785	1.00	36.96	200	N	ALA A 139	72.686	-13.513	-13.520	1.00	34.74
148	CB	MET A 131	73.143	5.484	-8.760	1.00	42.16	201	CA	ALA A 139	73.425	-12.724	-12.554	1.00	35.56
149	CG	MET A 131	74.218	4.719	-9.540	1.00	44.07	202	C	ALA A 139	73.532	-11.183	-12.677	1.00	35.73
150	SD	MET A 131	74.661	5.555	-11.071	1.00	48.37	203	O	ALA A 139	73.900	-10.477	-11.730	1.00	35.31
151	CE	MET A 131	76.298	6.126	-10.590	1.00	45.57	204	CB	ALA A 139	74.919	-13.209	-12.589	1.00	34.52
152	N	PRO A 132	70.445	3.644	-9.407	1.00	38.54	205	N	SER A 140	73.342	-10.684	-13.897	1.00	33.61
153	CA	PRO A 132	69.715	2.529	-9.985	1.00	38.36	206	CA	SER A 140	73.339	-9.259	-14.191	1.00	31.82

207	C	SER A 140	74.597	-8.519	-13.797	1.00	30.11	260	CB	LYS A 147	88.113	-11.724	0.937	1.00	35.09
208	O	SER A 140	74.538	-7.393	-13.302	1.00	28.60	261	CG	LYS A 147	87.594	-10.845	-0.194	1.00	37.87
209	CB	SER A 140	72.075	-8.690	-13.546	1.00	32.25	262	CD	LYS A 147	88.354	-9.540	-0.293	1.00	39.84
210	OG	SER A 140	71.767	-7.352	-13.873	1.00	33.30	263	CE	LYS A 147	88.103	-8.652	0.904	1.00	43.26
211	N	GLY A 141	75.769	-9.122	-13.958	1.00	30.48	264	NZ	LYS A 147	88.602	-7.248	0.739	1.00	45.31
212	CA	GLY A 141	77.065	-8.569	-13.643	1.00	29.15	265	N	THR A 148	88.360	-14.796	2.487	1.00	31.96
213	C	GLY A 141	77.524	-8.599	-12.198	1.00	30.03	266	CA	THR A 148	89.108	-15.593	3.444	1.00	30.46
214	O	GLY A 141	78.613	-8.120	-11.877	1.00	29.74	267	C	THR A 148	89.841	-16.711	2.711	1.00	32.06
215	N	PHE A 142	76.701	-9.126	-11.278	1.00	29.58	268	O	THR A 148	91.043	-16.921	2.873	1.00	30.77
216	CA	PHE A 142	77.047	-9.134	-9.867	1.00	27.65	269	CB	THR A 148	88.182	-16.136	4.545	1.00	28.74
217	C	PHE A 142	78.017	-10.281	-9.612	1.00	28.38	270	OG1	THR A 148	87.559	-15.026	5.205	1.00	25.09
218	O	PHE A 142	77.839	-11.354	-10.191	1.00	28.16	271	CG2	THR A 148	88.854	-16.928	5.658	1.00	29.31
219	CB	PHE A 142	75.796	-9.311	-8.977	1.00	25.35	272	N	THR A 149	89.131	-17.425	1.847	1.00	31.51
220	CG	PHE A 142	74.956	-8.071	-8.790	1.00	24.90	273	CA	THR A 149	89.650	-18.565	1.097	1.00	32.38
221	CD1	PHE A 142	75.222	-7.188	-7.760	1.00	25.18	274	C	THR A 149	90.032	-18.207	-0.336	1.00	34.28
222	CD2	PHE A 142	73.892	-7.778	-9.620	1.00	24.79	275	O	THR A 149	90.843	-18.860	-0.978	1.00	34.35
223	CE1	PHE A 142	74.496	-6.026	-7.579	1.00	25.01	276	CB	THR A 149	88.573	-19.672	1.002	1.00	31.79
224	CE2	PHE A 142	73.144	-6.628	-9.448	1.00	25.31	277	OG1	THR A 149	87.433	-19.098	0.347	1.00	31.53
225	CZ	PHE A 142	73.437	-5.749	-8.425	1.00	24.62	278	CG2	THR A 149	88.174	-20.139	2.387	1.00	31.56
226	N	THR A 143	78.971	-10.095	-8.696	1.00	28.09	279	N	GLY A 150	89.415	-17.156	-0.867	1.00	34.16
227	CA	THR A 143	79.811	-11.224	-8.292	1.00	29.96	280	CA	GLY A 150	89.621	-16.692	-2.232	1.00	35.07
228	C	THR A 143	79.908	-11.299	-6.764	1.00	28.75	281	C	GLY A 150	88.528	-17.240	-3.148	1.00	34.60
229	O	THR A 143	79.791	-10.273	-6.092	1.00	30.13	282	O	GLY A 150	88.453	-16.846	-4.298	1.00	34.70
230	CB	THR A 143	81.234	-11.093	-8.857	1.00	30.83	283	N	GLU A 151	87.706	-18.163	-2.651	1.00	34.79
231	OG1	THR A 143	81.625	-9.746	-8.536	1.00	32.43	284	CA	GLU A 151	86.647	-18.768	-3.457	1.00	36.01
232	CG2	THR A 143	81.348	-11.292	-10.365	1.00	31.64	285	C	GLU A 151	85.618	-17.746	-3.946	1.00	35.57
233	N	VAL A 144	80.192	-12.468	-6.219	1.00	27.73	286	O	GLU A 151	85.046	-16.957	-3.184	1.00	32.89
234	CA	VAL A 144	80.403	-12.603	-4.774	1.00	26.92	287	CB	GLU A 151	85.878	-19.866	-2.699	1.00	36.86
235	C	VAL A 144	81.718	-13.339	-4.556	1.00	27.73	288	CG	GLU A 151	84.457	-20.388	-2.912	1.00	39.81
236	O	VAL A 144	81.994	-14.337	-5.233	1.00	27.48	289	CD	GLU A 151	83.800	-21.357	-1.955	1.00	41.00
237	CB	VAL A 144	79.255	-13.330	-4.060	1.00	24.80	290	OE1	GLU A 151	83.941	-21.618	-0.761	1.00	20.00
238	CG1	VAL A 144	79.645	-13.759	-2.633	1.00	24.36	291	OE2	GLU A 151	82.953	-21.888	-2.659	1.00	20.00
239	CG2	VAL A 144	78.034	-12.421	-3.949	1.00	24.13	292	N	LYS A 152	85.373	-17.792	-5.258	1.00	34.10
240	N	ILE A 145	82.561	-12.879	-3.637	1.00	28.05	293	CA	LYS A 152	84.388	-16.920	-5.880	1.00	33.14
241	CA	ILE A 145	83.791	-13.551	-3.267	1.00	28.41	294	C	LYS A 152	83.100	-17.721	-5.895	1.00	32.88
242	C	ILE A 145	83.948	-13.647	-1.740	1.00	28.01	295	O	LYS A 152	83.174	-18.923	-6.156	1.00	34.46
243	O	ILE A 145	83.742	-12.756	-0.920	1.00	25.69	296	CB	LYS A 152	84.713	-16.397	-7.291	1.00	33.96
244	CB	ILE A 145	85.080	-12.944	-3.871	1.00	31.57	297	CG	LYS A 152	86.053	-15.890	-7.831	1.00	20.00
245	CG1	ILE A 145	85.020	-12.914	-5.399	1.00	34.81	298	CD	LYS A 152	86.300	-15.397	-9.258	1.00	20.00
246	CG2	ILE A 145	86.300	-13.815	-3.542	1.00	31.61	299	CE	LYS A 152	87.720	-14.878	-9.009	1.00	20.00
247	CD1	ILE A 145	85.691	-11.801	-6.162	0.00	38.05	300	NZ	LYS A 152	88.820	-14.900	-9.971	1.00	20.00
248	N	ASP A 146	84.373	-14.837	-1.350	1.00	25.58	301	N	ILE A 153	81.971	-17.105	-5.571	1.00	30.39
249	CA	ASP A 146	84.778	-15.165	0.006	1.00	28.42	302	CA	ILE A 153	80.697	-17.797	-5.515	1.00	30.58
250	C	ASP A 146	86.263	-14.824	-0.057	1.00	28.22	303	C	ILE A 153	79.766	-17.261	-6.561	1.00	30.18
251	O	ASP A 146	87.082	-15.643	-0.371	1.00	27.06	304	O	ILE A 153	79.369	-16.087	-6.544	1.00	29.54
252	CB	ASP A 146	84.462	-16.636	-0.239	1.00	26.87	305	CB	ILE A 153	80.079	-17.596	-4.102	1.00	30.99
253	CG	ASP A 146	84.854	-17.200	1.576	1.00	28.99	306	CG1	ILE A 153	81.005	-18.163	-3.015	1.00	32.60
254	OD1	ASP A 146	85.512	-16.536	2.398	1.00	27.91	307	CG2	ILE A 153	78.708	-18.243	-4.058	1.00	30.51
255	OD2	ASP A 146	84.521	-18.391	1.822	1.00	28.00	308	CD1	ILE A 153	80.665	-17.636	-1.620	1.00	33.71
256	N	LYS A 147	86.657	-13.694	0.591	1.00	29.63	309	N	PRO A 154	79.304	-18.086	-7.516	1.00	30.89
257	CA	LYS A 147	88.035	-13.237	0.631	1.00	33.19	310	CA	PRO A 154	78.425	-17.617	-8.577	1.00	29.91
258	C	LYS A 147	88.933	-14.018	1.577	1.00	33.69	311	C	PRO A 154	77.070	-17.092	-8.125	1.00	29.11
259	O	LYS A 147	90.160	-13.941	1.450	1.00	33.61	312	O	PRO A 154	76.389	-17.689	-7.291	1.00	28.76

313	CB	PRO A 154	78.239	-18.829	-9.471	1.00	30.32	366	ND2	ASN A 162	62.829	-0.625	-5.774	1.00	27.62
314	CG	PRO A 154	79.208	-19.853	-9.041	1.00	31.95	367	N	PRO A 163	58.979	3.767	-2.828	1.00	27.79
315	CD	PRO A 154	79.709	-19.499	-7.665	1.00	30.13	368	CA	PRO A 163	57.661	-4.372	-2.786	1.00	26.20
316	N	VAL A 155	76.635	-15.979	-8.687	1.00	29.63	369	C	PRO A 163	56.742	-3.804	-3.860	1.00	25.38
317	CA	VAL A 155	75.325	-15.376	-8.443	1.00	30.78	370	O	PRO A 163	56.967	-2.735	-4.449	1.00	24.29
318	CA	VAL A 155	74.378	-15.940	-9.509	1.00	30.85	371	CB	PRO A 163	57.181	-4.066	-1.369	1.00	27.88
319	O	VAL A 155	74.696	-15.745	-10.690	1.00	30.08	372	CG	PRO A 163	57.870	-2.776	-1.027	1.00	28.89
320	CB	VAL A 155	75.011	-13.871	-8.530	1.00	30.85	373	CD	PRO A 163	59.234	-2.875	-1.661	1.00	27.81
321	CG1	VAL A 155	73.895	-13.215	-8.115	1.00	20.00	374	N	VAL A 164	55.717	-4.569	-4.208	1.00	25.30
322	CG2	VAL A 155	76.117	-13.400	-7.604	1.00	29.33	375	CA	VAL A 164	54.721	-4.187	-5.220	1.00	25.51
323	N	THR A 156	73.320	-16.648	-9.159	1.00	29.83	376	C	VAL A 164	53.339	-4.283	-4.585	1.00	24.80
324	CA	THR A 156	72.450	-17.270	-10.144	1.00	31.67	377	O	VAL A 164	52.995	-5.340	-4.040	1.00	26.11
325	C	THR A 156	71.245	-16.427	-10.562	1.00	32.89	378	CB	VAL A 164	54.802	-5.048	-6.493	1.00	24.71
326	O	THR A 156	70.632	-16.699	-11.621	1.00	32.33	379	CG1	VAL A 164	53.663	-4.752	-7.467	1.00	26.19
327	CB	THR A 156	71.956	-18.634	-9.635	1.00	31.70	380	CG2	VAL A 164	56.125	-4.811	-7.253	1.00	25.42
328	CG1	THR A 156	71.092	-18.419	-8.515	1.00	31.91	381	N	THR A 165	52.538	-3.233	-4.606	1.00	24.33
329	CG2	THR A 156	73.150	-19.479	-9.186	1.00	32.24	382	CA	THR A 165	51.200	-3.270	-4.032	1.00	25.19
330	N	SER A 157	70.880	-15.436	-9.730	1.00	31.06	383	C	THR A 165	50.176	-3.008	-5.166	1.00	24.41
331	CA	SER A 157	69.833	-14.506	-10.141	1.00	30.56	384	O	THR A 165	49.956	-1.847	-5.503	1.00	21.40
332	C	SER A 157	69.803	-13.227	-9.308	1.00	29.60	385	CB	THR A 165	50.966	-2.262	-2.897	1.00	26.83
333	O	SER A 157	70.337	-13.169	-8.195	1.00	27.35	386	OG1	THR A 165	51.832	-2.523	-1.774	1.00	28.11
334	CB	SER A 157	68.491	-15.222	-10.214	1.00	32.34	387	CG2	THR A 165	49.533	-2.347	-2.377	1.00	25.74
335	OG	SER A 157	67.810	-15.173	-9.012	1.00	35.08	388	N	ALA A 166	49.546	-4.081	-5.643	1.00	22.25
336	N	ALA A 158	69.446	-12.117	-9.959	1.00	26.45	389	CA	ALA A 166	48.656	-3.909	-6.820	1.00	23.36
337	CA	ALA A 158	69.453	-10.774	-9.423	1.00	27.24	390	C	ALA A 166	47.323	-4.512	-6.453	1.00	22.56
338	C	ALA A 158	68.152	-10.053	-9.765	1.00	30.18	391	O	ALA A 166	47.351	-5.703	-6.108	1.00	24.73
339	O	ALA A 158	67.765	-9.918	-10.959	1.00	30.53	392	CB	ALA A 166	49.294	-4.589	-8.031	1.00	19.57
340	CB	ALA A 158	70.645	-10.022	-9.985	1.00	26.36	393	N	VAL A 167	46.229	-3.768	-6.464	1.00	22.47
341	N	VAL A 159	67.340	-9.812	-8.734	1.00	28.12	394	CA	VAL A 167	44.939	-4.309	-6.043	1.00	19.46
342	CA	VAL A 159	66.000	-9.269	-8.930	1.00	28.80	395	C	VAL A 167	43.980	-4.333	-7.248	1.00	21.03
343	C	VAL A 159	65.789	-8.029	-8.074	1.00	28.52	396	O	VAL A 167	43.901	-3.309	-7.917	1.00	18.72
344	O	VAL A 159	66.627	-7.709	-7.226	1.00	25.60	397	CB	VAL A 167	44.310	-3.476	-4.911	1.00	20.70
345	CB	VAL A 159	64.846	-10.243	-8.667	1.00	29.04	398	CG1	VAL A 167	42.832	-3.503	-4.525	1.00	18.70
346	CG1	VAL A 159	64.965	-11.513	-9.494	1.00	29.16	399	CG2	VAL A 167	45.155	-3.486	-3.651	1.00	22.11
347	CG2	VAL A 159	64.667	-10.636	-7.188	1.00	27.70	400	N	LEU A 168	43.264	-5.454	-7.447	1.00	19.41
348	N	SER A 160	64.643	-7.357	-8.283	1.00	28.60	401	CA	LEU A 168	42.257	-5.482	-8.519	1.00	18.94
349	CA	SER A 160	64.422	-6.159	-7.460	1.00	27.56	402	C	LEU A 168	41.053	-4.647	-8.099	1.00	20.89
350	O	SER A 160	63.738	-6.562	-6.141	1.00	27.31	403	O	LEU A 168	40.431	-4.955	-7.048	1.00	21.09
351	C	SER A 160	62.904	-7.468	-6.153	1.00	25.37	404	CB	LEU A 168	41.808	-6.925	-8.770	1.00	18.27
352	CB	SER A 160	63.626	-5.076	-8.149	1.00	28.21	405	CG	LEU A 168	40.646	-7.136	-9.739	1.00	18.57
353	OG	SER A 160	63.262	-4.072	-7.188	1.00	25.98	406	CD1	LEU A 168	41.115	-6.720	-11.135	1.00	17.67
354	N	ALA A 161	64.205	-5.955	-5.033	1.00	25.91	407	CD2	LEU A 168	40.166	-8.607	-9.767	1.00	17.71
355	CA	ALA A 161	63.629	-6.241	-3.731	1.00	25.68	408	N	VAL A 169	40.726	-3.598	-8.865	1.00	20.18
356	C	ALA A 161	62.547	-5.238	-3.329	1.00	26.62	409	CA	VAL A 169	39.571	-2.758	-8.519	1.00	19.68
357	O	ALA A 161	61.886	-5.395	-2.296	1.00	23.95	410	C	VAL A 169	38.501	-2.816	-9.592	1.00	20.02
358	CB	ALA A 161	64.715	-6.344	-2.642	1.00	25.65	411	O	VAL A 169	38.871	-2.925	-10.765	1.00	19.91
359	N	ASN A 162	62.257	-4.216	-4.131	1.00	26.84	412	CB	VAL A 169	39.943	-1.260	-8.324	1.00	19.72
360	CA	ASN A 162	61.183	-3.278	-3.763	1.00	27.62	413	CG1	VAL A 169	40.903	-1.142	-7.131	1.00	17.22
361	C	ASN A 162	59.841	-3.987	-3.818	1.00	28.07	414	CG2	VAL A 169	40.600	-0.612	-9.541	1.00	18.93
362	O	ASN A 162	59.547	-4.755	-4.741	1.00	28.17	415	N	GLY A 170	37.224	-2.742	-9.246	1.00	18.55
363	CB	ASN A 162	61.196	-2.092	-4.718	1.00	28.34	416	CA	GLY A 170	36.172	-2.790	-10.248	1.00	18.73
364	CG	ASN A 162	62.395	-1.174	-4.643	1.00	29.74	417	C	GLY A 170	34.791	-3.031	-9.664	1.00	17.66
365	OD1	ASN A 162	62.886	-0.911	-3.535	1.00	30.40	418	O	GLY A 170	34.639	-3.096	-8.438	1.00	17.25

419	N	ASP A 171	33.806	-3.317	-10.500	1.00	18.35	472	C	ALA A 178	34.509	-6.155	-0.321	1.00	33.76
420	CA	ASP A 171	32.470	-3.653	-10.006	1.00	22.28	473	O	ALA A 178	33.439	-6.440	-0.842	1.00	33.43
421	C	ASP A 171	32.356	-5.172	-9.771	1.00	22.87	474	CB	ALA A 178	36.359	-5.829	-1.970	1.00	32.96
422	O	ASP A 171	31.275	-5.671	-9.490	1.00	21.75	475	N	ALA A 179	34.601	-5.282	0.670	1.00	33.57
423	CB	ASP A 171	31.304	-3.164	-10.866	1.00	22.13	476	CA	ALA A 179	33.434	-4.614	1.223	1.00	32.22
424	CG	ASP A 171	31.364	-3.728	-12.276	1.00	24.79	477	C	ALA A 179	32.707	-3.731	0.213	1.00	30.62
425	OD1	ASP A 171	32.272	-4.532	-12.592	1.00	24.08	478	O	ALA A 179	31.466	-3.697	0.192	1.00	30.86
426	OD2	ASP A 171	30.463	-3.373	-13.068	1.00	25.44	479	CB	ALA A 179	33.856	-3.733	2.401	1.00	34.25
427	N	LEU A 172	33.459	-5.907	-9.824	1.00	23.38	480	N	ASN A 180	33.420	-2.907	-0.561	1.00	29.04
428	CA	LEU A 172	33.556	-7.317	-9.519	1.00	23.45	481	CA	ASN A 180	32.851	-2.015	-1.558	1.00	28.58
429	C	LEU A 172	34.101	-7.426	-8.093	1.00	23.46	482	C	ASN A 180	33.499	-2.211	-2.939	1.00	27.39
430	O	LEU A 172	34.338	-8.531	-7.601	1.00	23.89	483	O	ASN A 180	34.638	-2.689	-3.042	1.00	26.95
431	CB	LEU A 172	34.488	-8.066	-10.492	1.00	23.96	484	CB	ASN A 180	32.957	-0.521	-1.148	1.00	29.90
432	CG	LEU A 172	35.716	-7.388	-11.089	1.00	23.60	485	CG	ASN A 180	32.103	-0.258	0.104	1.00	31.68
433	CD1	LEU A 172	36.700	-6.874	-10.024	1.00	23.92	486	OD1	ASN A 180	30.885	-0.552	0.100	1.00	34.34
434	CD2	LEU A 172	36.501	-8.286	-12.049	1.00	22.64	487	OD2	ASN A 180	32.750	0.063	1.209	1.00	32.41
435	N	GLN A 173	34.427	-6.304	-7.425	1.00	22.02	488	N	ASN A 181	32.825	-1.832	-4.017	1.00	25.75
436	CA	GLN A 173	35.116	-6.409	-6.144	1.00	23.00	489	CA	ASN A 181	33.370	-1.875	-5.372	1.00	25.22
437	C	GLN A 173	34.301	-7.061	-5.012	1.00	25.30	490	C	ASN A 181	34.287	-0.683	-5.625	1.00	24.74
438	O	GLN A 173	34.956	-7.770	-4.222	1.00	23.45	491	O	ASN A 181	34.253	0.299	-4.849	1.00	23.10
439	CB	GLN A 173	35.715	-5.085	-5.640	1.00	19.82	492	CB	ASN A 181	32.221	-1.881	-6.393	1.00	24.36
440	CG	GLN A 173	37.222	-5.133	-5.502	1.00	20.64	493	CG	ASN A 181	31.526	-3.216	-6.503	1.00	23.81
441	CD	GLN A 173	37.865	-3.790	-5.190	1.00	20.89	494	OD1	ASN A 181	30.312	-3.231	-6.776	1.00	25.93
442	OE1	GLN A 173	38.776	-3.712	-4.337	1.00	21.68	495	ND2	ASN A 181	32.208	-4.326	-6.339	1.00	19.94
443	NE2	GLN A 173	37.472	-2.762	-5.917	1.00	14.10	496	N	TRP A 182	35.132	-0.743	-6.657	1.00	20.37
444	N	GLN A 174	33.011	-6.766	-4.897	1.00	27.15	497	CA	TRP A 182	36.096	0.317	-6.986	1.00	22.89
445	CA	GLN A 174	32.211	-7.350	-3.808	1.00	30.17	498	C	TRP A 182	36.812	0.884	-5.748	1.00	24.90
446	C	GLN A 174	32.010	-8.853	-3.980	1.00	29.95	499	O	TRP A 182	36.686	2.061	-5.356	1.00	22.19
447	O	GLN A 174	32.162	-9.617	-3.030	1.00	29.74	500	CB	TRP A 182	35.440	1.390	-7.842	1.00	21.88
448	CB	GLN A 174	30.806	-6.738	-3.686	1.00	30.31	501	CG	TRP A 182	34.968	0.888	-9.213	1.00	21.19
449	CG	GLN A 174	30.791	-5.300	-3.184	1.00	31.02	502	CD1	TRP A 182	33.661	0.662	-9.556	1.00	20.22
450	CD	GLN A 174	29.381	-4.727	-3.153	1.00	32.11	503	CD2	TRP A 182	35.772	0.587	-10.354	1.00	20.33
451	OE1	GLN A 174	28.641	-4.750	-4.123	1.00	32.20	504	NE1	TRP A 182	33.620	0.238	-10.890	1.00	21.14
452	NE2	GLN A 174	29.058	-4.103	-2.011	1.00	32.45	505	CE2	TRP A 182	34.899	0.206	-11.396	1.00	20.92
453	N	ALA A 175	31.859	-9.290	-5.225	1.00	30.17	506	CE3	TRP A 182	37.140	0.646	-10.652	1.00	19.83
454	CA	ALA A 175	31.793	-10.722	-5.537	1.00	30.64	507	CZ2	TRP A 182	35.335	-0.126	-12.679	1.00	19.37
455	C	ALA A 175	33.072	-11.450	-5.174	1.00	30.81	508	CZ3	TRP A 182	37.588	0.290	-11.911	1.00	20.08
456	O	ALA A 175	33.044	-12.667	-4.926	1.00	31.59	509	CH2	TRP A 182	36.682	-0.111	-12.925	1.00	18.62
457	CB	ALA A 175	31.469	-10.864	-7.023	1.00	30.89	510	N	SER A 183	37.553	-0.028	-5.091	1.00	24.20
458	N	LEU A 176	34.188	-10.738	-5.050	1.00	29.83	511	CA	SER A 183	38.166	0.298	-3.787	1.00	25.99
459	CA	LEU A 176	35.474	-11.299	-4.683	1.00	30.69	512	C	SER A 183	39.619	-0.056	-3.755	1.00	25.00
460	C	LEU A 176	35.799	-11.058	-3.218	1.00	31.12	513	O	SER A 183	40.038	-1.222	-3.552	1.00	24.72
461	O	LEU A 176	36.912	-11.315	-2.771	1.00	31.07	514	CB	SER A 183	37.250	-0.396	-2.744	1.00	27.68
462	CB	LEU A 176	36.587	-10.806	-5.622	1.00	30.20	515	OG	SER A 183	37.806	-0.303	-1.422	1.00	31.94
463	CG	LEU A 176	36.490	-11.210	-7.098	1.00	30.54	516	N	PRO A 184	40.504	0.901	-3.999	1.00	24.27
464	CD1	LEU A 176	37.534	-10.515	-7.971	1.00	28.99	517	CA	PRO A 184	41.936	0.660	-4.076	1.00	25.54
465	CD2	LEU A 176	36.726	-12.713	-7.263	1.00	30.40	518	C	PRO A 184	42.583	0.218	-2.771	1.00	27.63
466	N	GLY A 177	34.829	-10.590	-2.432	1.00	33.38	519	O	PRO A 184	43.702	-0.312	-2.819	1.00	26.74
467	CA	GLY A 177	34.977	-10.426	-1.004	1.00	34.48	520	CB	PRO A 184	42.567	2.002	-4.480	1.00	25.19
468	C	GLY A 177	35.277	-9.040	-0.468	1.00	36.08	521	CG	PRO A 184	41.436	2.850	-4.939	1.00	27.00
469	O	GLY A 177	35.331	-8.865	0.764	1.00	35.24	522	CD	PRO A 184	40.171	2.317	-4.293	1.00	25.48
470	N	ALA A 178	35.543	-8.079	-1.354	1.00	34.40	523	N	ASP A 185	41.953	0.501	-1.660	1.00	28.67
471	CA	ALA A 178	35.818	-6.733	-0.871	1.00	34.80	524	CA	ASP A 185	42.469	0.243	-0.330	1.00	35.01

C	ASP A 185	42.168	-1.154	0.186	1.00	32.77	578	CD1 LEU A 191	45.698	-8.077	-8.268	1.00	18.64
C525	ASP A 185	42.631	-1.481	1.276	1.00	32.78	579	CD2 LEU A 191	47.599	-8.457	-9.886	1.00	21.63
C526	ASP A 185	41.794	1.331	0.575	1.00	40.22	580	CD3 LEU A 192	48.898	-11.403	-5.497	1.00	23.59
C528	CG ASP A 185	40.328	0.971	0.823	1.00	45.75	581	CA LYS A 192	50.006	-12.052	-4.827	1.00	24.86
C529	OD1 ASP A 185	39.796	-0.145	0.631	1.00	49.67	582	C LYS A 192	51.232	-12.227	-5.700	1.00	26.50
C530	OD2 ASP A 185	39.665	1.968	1.250	1.00	48.92	583	O LYS A 192	51.100	-12.428	-6.912	1.00	26.86
C531	N ASP A 186	41.216	-1.836	-0.471	1.00	30.11	584	CB LYS A 192	49.560	-13.491	-4.421	1.00	25.31
C532	CA ASP A 186	40.727	-3.109	0.072	1.00	29.50	585	CG LYS A 192	47.815	-14.750	-3.079	0.00	20.00
C533	O ASP A 186	41.595	-4.279	-0.355	1.00	28.84	587	CE LYS A 192	46.420	-14.700	-2.448	0.00	20.00
C534	C ASP A 186	41.578	-4.767	-1.473	1.00	26.82	588	NZ LYS A 192	46.039	-16.034	-1.988	0.00	20.00
C535	CB ASP A 186	39.253	-3.271	-0.280	1.00	29.89	588	N LYS A 193	52.413	-12.326	-5.098	1.00	27.68
C536	CG ASP A 186	38.521	-4.309	0.548	1.00	30.33	589	N LYS A 193	53.593	-12.532	-5.943	1.00	32.22
C537	OD1 ASP A 186	39.135	-5.357	0.847	1.00	30.32	590	CA LYS A 193	53.825	-13.987	-6.288	1.00	32.50
C538	OD2 ASP A 186	37.337	-4.120	0.897	1.00	29.44	591	C LYS A 193	53.939	-14.822	-5.409	1.00	30.76
C539	N ASP A 187	42.390	-4.757	0.617	1.00	28.04	592	O LYS A 193	54.734	-11.805	-5.260	1.00	35.25
C540	CA ASP A 187	43.314	-5.849	0.376	1.00	28.05	593	CB LYS A 193	56.021	-12.513	-4.979	1.00	39.64
C541	C ASP A 187	42.680	-7.218	0.204	1.00	26.64	594	CG LYS A 193	57.217	-11.595	-5.033	1.00	41.28
C542	O ASP A 187	43.469	-8.146	0.051	1.00	26.92	595	CD LYS A 193	58.106	-11.653	-3.808	1.00	44.51
C543	CB ASP A 187	44.447	-5.977	1.403	1.00	29.12	596	CE LYS A 193	59.154	-10.583	-3.791	1.00	45.93
C544	CG ASP A 187	45.562	-5.006	1.075	1.00	29.66	597	NZ LYS A 193	53.836	-14.305	-7.593	1.00	30.97
C545	OD1 ASP A 187	45.560	-4.414	-0.035	1.00	29.31	598	N ILE A 194	54.161	-15.631	-8.117	1.00	29.28
C546	OD2 ASP A 187	46.419	-4.719	1.940	1.00	30.32	599	CA ILE A 194	55.654	-15.716	-8.412	1.00	28.94
C547	N HTS A 188	41.382	-7.380	0.101	1.00	25.81	600	C ILE A 194	56.334	-16.725	-8.177	1.00	28.26
C548	CA HTS A 188	40.750	-8.635	-0.234	1.00	28.57	601	O ILE A 194	53.341	-15.917	-9.394	1.00	30.80
C549	C HTS A 188	41.034	-8.980	-1.719	1.00	28.04	602	CB ILE A 194	51.872	-15.560	-9.172	1.00	29.46
C550	O HTS A 188	40.988	-10.162	-2.051	1.00	25.11	603	CG1 ILE A 194	53.505	-17.363	-9.869	1.00	30.31
C551	CB HTS A 188	39.247	-8.622	0.001	1.00	31.30	604	CG2 ILE A 194	51.129	-16.279	-8.076	1.00	29.66
C552	CG HTS A 188	38.773	-8.598	1.420	1.00	35.25	605	CD1 ILE A 194	56.246	-14.658	-8.969	1.00	26.41
C553	ND1 HTS A 188	38.178	-9.695	2.019	1.00	36.56	606	N ASN A 195	57.689	-14.582	-9.209	1.00	25.15
C554	CD2 HTS A 188	38.785	-7.621	2.366	1.00	36.05	607	CA ASN A 195	57.982	-13.108	-9.056	1.00	25.32
C555	CE1 HTS A 188	37.843	-9.392	3.263	1.00	37.12	608	C ASN A 195	57.060	-12.285	-9.010	1.00	24.84
C556	NE2 HTS A 188	38.209	-8.137	3.496	1.00	38.08	609	O ASN A 195	58.205	-15.255	-10.468	1.00	26.01
C557	N THR A 189	41.419	-8.003	-2.549	1.00	25.78	610	CB ASN A 195	58.002	-14.588	-11.816	1.00	23.49
C558	CA THR A 189	41.749	-8.277	-3.944	1.00	25.63	611	CG ASN A 195	58.324	-13.419	-11.979	1.00	22.62
C559	C THR A 189	43.164	-7.831	-4.295	1.00	26.53	612	OD1 ASN A 195	57.463	-15.271	-12.821	1.00	21.61
C560	O THR A 189	43.525	-7.508	-5.446	1.00	25.53	613	ND2 ASN A 195	59.232	-12.681	-8.921	1.00	27.18
C561	CB THR A 189	40.736	-7.696	-4.945	1.00	24.83	614	N PRO A 196	59.566	-11.282	-8.695	1.00	27.81
C562	CG1 THR A 189	40.551	-6.312	-4.648	1.00	23.22	615	CA PRO A 196	59.014	-10.304	-9.712	1.00	28.82
C563	CG2 THR A 189	39.397	-8.428	-4.913	1.00	24.10	616	C PRO A 196	58.874	-9.118	-9.403	1.00	29.64
C564	N LEU A 190	44.036	-7.871	-3.278	1.00	24.47	617	O PRO A 196	61.088	-11.245	-8.660	1.00	27.55
C565	CA LEU A 190	45.446	-7.592	-3.497	1.00	25.02	618	CB PRO A 196	61.562	-12.641	-8.735	1.00	27.24
C566	C LEU A 190	46.106	-8.740	-4.276	1.00	25.66	619	CG PRO A 196	60.400	-13.571	-8.910	1.00	27.99
C567	O LEU A 190	45.947	-9.871	-3.821	1.00	24.54	620	CD PRO A 196	58.728	-10.737	-10.939	1.00	28.40
C568	CB LEU A 190	46.115	-7.493	-2.126	1.00	25.49	621	N ASN A 197	58.152	-9.868	-11.964	1.00	27.61
C569	CG LEU A 190	47.612	-7.221	-2.066	1.00	26.63	622	CA ASN A 197	56.808	-10.412	-12.426	1.00	26.54
C570	CD1 LEU A 190	47.961	-5.811	-2.561	1.00	26.87	623	C ASN A 197	56.446	-10.216	-13.588	1.00	24.74
C571	CD2 LEU A 190	48.107	-7.483	-0.649	1.00	26.92	624	O ASN A 197	59.156	-9.685	-13.114	1.00	25.82
C572	N LEU A 191	46.785	-8.501	-5.397	1.00	23.25	625	CB ASN A 197	58.874	-8.553	-14.073	1.00	24.90
C573	CA LEU A 191	47.424	-9.589	-6.120	1.00	22.73	626	CG ASN A 197	58.401	-7.487	-13.679	1.00	25.87
C574	C LEU A 191	48.627	-10.118	-5.353	1.00	23.44	627	OD1 ASN A 197	59.143	-8.694	-15.374	1.00	22.51
C575	O LEU A 191	49.390	-9.351	-4.748	1.00	21.57	628	ND2 ASN A 197	56.003	-11.008	-11.527	1.00	25.03
C576	CB LEU A 191	47.921	-9.125	-7.510	1.00	21.62	629	N LEU A 198	54.709	-11.567	-11.921	1.00	25.50
C577	CG LEU A 191	46.880	-8.960	-8.614	1.00	21.93	630	CA LEU A 198					

631	C	LEU A 198	53.734	-11.604	-10.757	1.00	24.75	32.594	-14.705	-10.324	1.00	27.14
632	O	LEU A 198	54.037	-12.353	-9.805	1.00	24.83	31.303	-15.289	-10.898	1.00	29.05
633	CB	LEU A 198	54.639	-12.947	-12.600	1.00	26.19	31.325	-16.121	-11.802	1.00	27.54
634	CG	LEU A 198	53.385	-13.711	-13.032	1.00	29.17	33.139	-13.666	-11.307	1.00	27.39
635	CD1	LEU A 198	52.653	-13.174	-14.263	1.00	28.46	34.340	-12.803	-10.896	1.00	27.95
636	CD2	LEU A 198	54.064	-15.009	-13.469	1.00	31.33	34.858	-12.022	-12.101	1.00	27.28
637	N	TYR A 199	52.635	-10.883	-10.781	1.00	22.56	33.999	-11.861	-9.743	1.00	29.19
638	CA	TYR A 199	51.640	-10.794	-9.724	1.00	22.64	30.154	-14.795	-10.441	1.00	30.40
639	O	TYR A 199	50.281	-11.275	-10.192	1.00	23.37	28.870	-15.199	-11.005	1.00	30.93
640	C	TYR A 199	49.898	-10.900	-11.326	1.00	21.85	28.882	-14.794	-12.473	1.00	31.99
641	CB	TYR A 199	51.488	-9.332	-9.172	1.00	22.41	29.702	-13.916	-12.809	1.00	32.25
642	CG	TYR A 199	52.673	-9.037	-8.251	1.00	24.19	27.830	-14.370	-10.241	1.00	30.06
643	CD1	TYR A 199	52.525	-9.019	-6.870	1.00	24.33	28.518	-13.896	-9.020	1.00	30.95
644	CD2	TYR A 199	53.955	-8.856	-8.753	1.00	24.63	30.006	-13.818	-9.345	1.00	31.23
645	CE1	TYR A 199	53.599	-8.782	-6.021	1.00	23.22	27.959	-15.236	-13.292	1.00	30.94
646	CE2	TYR A 199	55.047	-8.650	-7.934	1.00	24.30	27.829	-14.752	-14.647	1.00	32.79
647	CZ	TYR A 199	54.848	-8.607	-6.552	1.00	25.35	27.525	-13.250	-14.646	1.00	33.93
648	OH	TYR A 199	55.967	-8.424	-5.758	1.00	25.36	26.875	-12.784	-13.698	1.00	33.84
649	N	GLN A 200	49.593	-12.153	-9.437	1.00	21.46	26.644	-15.405	-15.344	1.00	33.37
650	CA	GLN A 200	48.319	-12.703	-9.851	1.00	22.78	27.891	-12.554	-15.717	1.00	33.30
651	C	GLN A 200	47.308	-12.901	-8.709	1.00	23.92	27.627	-11.117	-15.815	1.00	33.40
652	O	GLN A 200	47.642	-12.965	-7.529	1.00	23.20	28.764	-10.431	-16.590	1.00	34.81
653	CB	GLN A 200	48.460	-14.071	-10.554	1.00	23.72	29.748	-11.089	-16.954	1.00	34.75
654	CG	GLN A 200	49.326	-14.123	-11.818	1.00	24.08	28.631	-9.147	-16.855	1.00	33.68
655	CD	GLN A 200	49.357	-15.468	-12.509	1.00	24.08	29.649	-8.364	-17.553	1.00	35.01
656	CE1	GLN A 200	48.907	-15.563	-13.665	1.00	25.79	30.168	-7.337	-16.549	1.00	32.85
657	NE2	GLN A 200	49.802	-16.529	-11.838	1.00	21.68	29.371	-6.687	-15.843	1.00	31.81
658	N	LEU A 201	46.029	-12.854	-9.068	1.00	22.79	29.126	-7.714	-18.837	1.00	37.54
659	CA	LEU A 201	44.878	-13.063	-8.223	1.00	23.86	30.036	-6.711	-19.353	1.00	40.79
660	C	LEU A 201	43.871	-13.926	-8.993	1.00	22.76	27.808	-7.044	-18.521	1.00	38.82
661	O	LEU A 201	43.615	-13.595	-10.149	1.00	20.39	31.475	-7.356	-16.327	1.00	28.47
662	CB	LEU A 201	44.180	-11.770	-7.798	1.00	24.31	32.119	-6.499	-15.331	1.00	25.61
663	CG	LEU A 201	42.984	-11.871	-6.855	1.00	27.82	33.148	-5.574	-15.968	1.00	23.20
664	CD1	LEU A 201	43.423	-12.292	-5.451	1.00	28.00	33.511	-5.730	-17.129	1.00	20.43
665	CD2	LEU A 201	42.247	-10.531	-6.725	1.00	26.81	32.853	-7.361	-14.285	1.00	25.13
666	N	SER A 202	43.269	-14.938	-8.367	1.00	21.06	32.043	-8.437	-13.604	1.00	25.77
667	CA	SER A 202	42.217	-15.727	-8.956	1.00	20.94	31.418	-8.187	-12.385	1.00	26.19
668	C	SER A 202	40.969	-15.724	-8.085	1.00	24.18	31.878	-9.699	-14.159	1.00	26.65
669	O	SER A 202	41.140	-15.747	-6.843	1.00	26.01	30.647	-9.141	-11.755	1.00	25.94
670	CB	SER A 202	42.700	-17.198	-9.057	1.00	21.57	31.129	-10.686	-13.531	1.00	26.59
671	OG	SER A 202	43.669	-17.342	-10.101	1.00	24.54	30.508	-10.392	-12.330	1.00	27.30
672	N	GLY A 203	39.768	-15.823	-8.623	1.00	24.80	29.776	-11.352	-11.675	1.00	28.27
673	CA	GLY A 203	38.565	-15.892	-7.834	1.00	25.89	33.707	-4.664	-15.180	1.00	21.51
674	C	GLY A 203	37.359	-16.159	-8.711	1.00	28.12	34.770	-3.769	-15.611	1.00	21.91
675	O	GLY A 203	37.385	-15.914	-9.919	1.00	28.11	35.851	-3.700	-14.517	1.00	20.11
676	N	THR A 204	36.305	-16.716	-8.088	1.00	27.74	35.444	-3.737	-13.367	1.00	19.22
677	CA	THR A 204	35.097	-17.110	-8.779	1.00	26.86	34.270	-2.358	-15.949	1.00	20.26
678	C	THR A 204	34.105	-15.971	-8.927	1.00	26.50	33.515	-2.252	-17.274	1.00	21.03
679	O	THR A 204	33.813	-15.312	-7.936	1.00	26.91	32.948	-0.889	-17.595	1.00	21.84
680	CB	THR A 204	34.383	-18.207	-7.933	1.00	29.21	32.192	-0.698	-18.590	1.00	23.95
681	OG1	THR A 204	35.262	-19.322	-7.816	1.00	28.46	33.387	0.136	-16.876	1.00	20.75
682	CG2	THR A 204	33.059	-18.617	-8.581	1.00	28.38	37.144	-3.613	-14.861	1.00	18.80
683	N	LEU A 205	33.575	-15.738	-10.119	1.00	25.28	38.126	-3.616	-13.782	1.00	19.43



843	CD2	TYR	A	224	49.429	1.488	-16.013	1.00	22.63	896	N	THR	A	232	33.400	-10.266	-19.692	1.00	30.00
844	CE1	TYR	A	224	50.582	1.159	-13.505	1.00	22.51	897	CA	THR	A	232	32.070	-10.894	-19.612	1.00	32.54
845	CE2	TYR	A	224	50.582	2.186	-15.685	1.00	23.45	898	C	THR	A	232	32.246	-12.342	-19.188	1.00	32.86
846	CZ	TYR	A	224	51.161	2.018	-14.440	1.00	23.93	899	O	THR	A	232	33.069	-13.072	-19.750	1.00	32.67
847	OH	TYR	A	224	52.340	2.665	-14.126	1.00	26.78	900	CB	THR	A	232	31.143	-10.753	-20.806	1.00	33.54
848	N	PRO	A	225	44.910	-0.545	-16.957	1.00	23.50	901	OG1	THR	A	232	31.043	-11.964	-21.567	1.00	37.56
849	CA	PRO	A	225	45.501	0.350	-17.935	1.00	22.64	902	OG2	THR	A	232	31.478	-9.607	-21.734	1.00	30.68
850	C	PRO	A	225	44.900	1.756	-17.867	1.00	22.45	903	N	VAL	A	233	31.540	-12.713	-18.135	1.00	33.79
851	O	PRO	A	225	44.313	2.161	-16.872	1.00	21.99	904	CA	VAL	A	233	31.579	-14.068	-17.613	1.00	36.22
852	CB	PRO	A	225	45.385	-0.335	-19.294	1.00	23.11	905	C	VAL	A	233	30.298	-14.809	-17.947	1.00	38.71
853	CG	PRO	A	225	44.382	-1.484	-19.173	1.00	23.73	906	O	VAL	A	233	29.186	-14.331	-17.740	1.00	37.77
854	CD	PRO	A	225	43.979	-1.435	-17.622	1.00	22.80	907	CB	VAL	A	233	31.792	-13.955	-16.105	1.00	35.04
855	N	GLY	A	226	45.077	2.458	-19.001	1.00	21.76	908	CG1	VAL	A	233	31.838	-15.338	-15.489	1.00	35.88
856	CA	GLY	A	226	44.559	3.812	-19.040	1.00	21.93	909	CG2	VAL	A	233	33.107	-13.252	-15.847	1.00	33.72
857	C	GLY	A	226	43.022	3.923	-19.125	1.00	23.76	910	N	PRO	A	234	30.486	-16.031	-18.513	1.00	41.11
858	O	GLY	A	226	42.405	4.932	-18.809	1.00	23.80	911	CA	PRO	A	234	29.393	-16.841	-19.027	1.00	42.50
859	N	ASN	A	227	42.466	2.802	-19.616	1.00	23.49	912	C	PRO	A	234	28.491	-17.443	-17.947	1.00	43.33
860	CA	ASN	A	227	41.018	2.737	-19.670	1.00	24.79	913	O	PRO	A	234	28.940	-17.865	-16.889	1.00	45.44
861	C	ASN	A	227	40.364	1.416	-18.959	1.00	23.66	914	CB	PRO	A	234	29.993	-18.031	-19.783	1.00	41.71
862	O	ASN	A	227	41.160	0.489	-18.779	1.00	21.15	915	CG	PRO	A	234	31.509	-17.862	-19.793	1.00	42.81
863	CB	ASN	A	227	40.210	2.594	-21.106	1.00	26.98	916	CD	PRO	A	234	31.725	-16.769	-18.640	1.00	42.19
864	CG	ASN	A	227	40.485	3.892	-21.877	1.00	29.55	917	N	GLN	A	235	27.199	-17.504	-18.314	1.00	20.00
865	OD1	ASN	A	227	40.418	4.994	-21.332	1.00	31.48	918	CA	GLN	A	235	26.246	-18.000	-17.341	1.00	20.00
866	ND2	ASN	A	227	40.823	3.724	-23.148	1.00	31.22	919	C	GLN	A	235	26.543	-19.290	-16.567	1.00	20.00
867	N	ASN	A	228	39.094	1.377	-18.571	1.00	23.20	920	O	GLN	A	235	26.691	-20.364	-17.135	1.00	20.00
868	CA	ASN	A	228	38.573	0.197	-17.841	1.00	22.62	921	CB	GLN	A	235	24.891	-18.189	-18.091	0.00	20.00
869	C	ASN	A	228	38.683	-1.049	-19.724	1.00	22.14	922	CG	GLN	A	235	23.744	-18.642	-17.182	0.00	20.00
870	O	ASN	A	228	38.483	-0.972	-19.949	1.00	21.31	923	CD	GLN	A	235	22.488	-18.822	-18.002	0.00	20.00
871	CB	ASN	A	228	37.100	0.435	-17.487	1.00	21.69	924	OE1	GLN	A	235	21.427	-19.185	-17.522	0.00	20.00
872	CG1	ASN	A	228	36.803	1.486	-16.423	1.00	21.12	925	NE2	GLN	A	235	22.653	-18.554	-19.313	0.00	20.00
873	OD1	ASN	A	228	35.598	1.769	-16.125	1.00	20.53	926	N	GLY	A	236	26.571	-19.113	-15.235	1.00	20.00
874	ND2	ASN	A	228	37.794	2.076	-15.831	1.00	18.06	927	CA	GLY	A	236	26.914	-20.255	-14.411	1.00	20.00
875	N	VAL	A	229	38.857	-2.232	-18.162	1.00	22.54	928	C	GLY	A	236	28.215	-19.843	-13.723	1.00	20.00
876	CA	VAL	A	229	38.894	-3.464	-18.981	1.00	20.25	929	O	GLY	A	236	28.571	-20.322	-12.660	1.00	20.00
877	C	VAL	A	229	37.524	-4.125	-18.851	1.00	20.80	930	N	GLY	A	237	28.951	-18.960	-14.432	1.00	45.11
878	O	VAL	A	229	37.078	-4.359	-17.734	1.00	20.94	931	CA	GLY	A	237	31.386	-19.060	-14.065	1.00	41.23
879	CB	VAL	A	229	39.990	-4.473	-18.584	1.00	19.95	932	C	GLY	A	237	31.412	-20.077	-14.716	1.00	41.47
880	CG1	VAL	A	229	39.902	-5.771	-19.415	1.00	14.74	933	O	GLY	A	237	32.494	-18.495	-13.570	1.00	39.53
881	CG2	VAL	A	229	41.389	-3.855	-18.689	1.00	15.89	934	N	GLU	A	238	33.738	-19.269	-13.544	1.00	36.93
882	N	SER	A	230	36.894	-4.469	-19.964	1.00	22.94	935	CA	GLU	A	238	34.814	-18.623	-12.658	1.00	35.69
883	CA	SER	A	230	35.595	-5.158	-19.969	1.00	22.94	936	C	GLU	A	238	34.687	-17.510	-12.178	1.00	34.73
884	C	SER	A	230	35.778	-6.674	-19.896	1.00	24.31	937	O	GLU	A	238	34.249	-19.376	-14.974	1.00	37.46
885	O	SER	A	230	36.593	-7.269	-20.616	1.00	21.95	938	CB	GLU	A	238	34.152	-18.042	-15.715	1.00	38.60
886	CB	SER	A	230	34.819	-4.769	-21.221	1.00	24.67	939	CG	GLU	A	238	34.928	-18.141	-17.002	1.00	38.06
887	OG	SER	A	230	33.548	-5.431	-21.269	1.00	28.19	940	CD	GLU	A	238	36.045	-17.645	-17.053	1.00	39.51
888	N	LEU	A	231	35.049	-7.328	-18.993	1.00	24.99	941	OE1	GLU	A	238	34.397	-18.708	-17.948	1.00	39.63
889	CA	LEU	A	231	35.108	-8.754	-18.760	1.00	26.33	942	OE2	GLU	A	238	35.917	-19.366	-12.434	1.00	31.34
890	C	LEU	A	231	33.709	-9.391	-18.724	1.00	29.37	943	N	LYS	A	239	36.752	-18.708	-12.071	1.00	30.50
891	O	LEU	A	231	32.966	-9.135	-17.764	1.00	28.67	944	CA	LYS	A	239	38.005	-18.078	-12.734	1.00	29.49
892	CB	LEU	A	231	35.779	-9.047	-17.422	1.00	25.50	945	C	LYS	A	239	38.644	-18.729	-13.541	1.00	26.10
893	CG	LEU	A	231	35.801	-10.449	-16.823	1.00	26.01	946	O	LYS	A	239	37.649	-19.635	-11.230	1.00	30.57
894	CD1	LEU	A	231	36.671	-11.424	-17.607	1.00	25.54	947	CB	LYS	A	239	39.081	-19.338	-10.780	1.00	32.75
895	CD2	LEU	A	231	36.348	-10.425	-15.384	1.00	25.86	948	CG	LYS	A	239					



949	CD	LYS	A	239	39.203	-19.871	-9.351	1.00	35.35	1002	CG2	ILE	A	245	55.434	-8.035	-16.554	1.00	18.24
950	CE	LYS	A	239	39.279	-21.314	-8.840	1.00	36.50	1003	CD1	ILE	A	245	53.736	-10.007	-17.795	1.00	27.43
951	NZ	LYS	A	239	39.762	-21.354	-7.461	1.00	33.54	1004	N	PRO	A	246	54.950	-6.024	-13.382	1.00	23.34
952	N	VAL	A	240	38.248	-16.787	-12.495	1.00	26.95	1005	CA	PRO	A	246	55.533	-4.759	-12.930	1.00	23.67
953	CA	VAL	A	240	39.095	-15.992	-13.399	1.00	23.70	1006	C	PRO	A	246	56.506	-4.124	-13.911	1.00	22.46
954	C	VAL	A	240	40.419	-15.640	-12.743	1.00	25.44	1007	O	PRO	A	246	56.416	-2.914	-14.115	1.00	22.69
955	O	VAL	A	240	40.437	-15.350	-11.538	1.00	23.90	1008	CB	PRO	A	246	56.242	-5.151	-11.622	1.00	23.64
956	CB	VAL	A	240	38.369	-14.708	-13.849	1.00	22.65	1009	CG	PRO	A	246	55.416	-6.302	-11.119	1.00	22.55
957	CG1	VAL	A	240	39.170	-13.901	-14.866	1.00	22.07	1010	CD	PRO	A	246	55.177	-7.102	-12.400	1.00	23.30
958	CG2	VAL	A	240	36.957	-14.947	-14.404	1.00	21.34	1011	N	SER	A	247	57.418	-4.864	-14.543	1.00	21.20
959	N	THR	A	241	41.505	-15.654	-13.524	1.00	24.76	1012	CA	SER	A	247	57.762	-3.511	-16.663	1.00	24.65
960	CA	THR	A	241	42.835	-15.308	-13.067	1.00	26.11	1013	C	SER	A	247	58.360	-4.243	-15.475	1.00	23.73
961	C	THR	A	241	43.244	-13.957	-13.689	1.00	26.23	1014	O	SER	A	247	58.408	-5.238	-16.041	1.00	24.40
962	O	THR	A	241	43.165	-13.786	-14.922	1.00	24.94	1015	CB	SER	A	247	58.758	-6.211	-16.858	1.00	23.42
963	CB	THR	A	241	43.856	-16.397	-13.451	1.00	26.92	1016	OG	SER	A	247	56.656	-3.993	-17.221	1.00	23.41
964	OG1	THR	A	241	43.594	-17.610	-12.693	1.00	29.26	1017	N	THR	A	248	56.010	-3.307	-18.332	1.00	23.91
965	CG2	THR	A	241	45.285	-15.969	-13.169	1.00	25.11	1018	CA	THR	A	248	54.887	-2.852	-17.942	1.00	23.60
966	N	PHE	A	242	43.659	-13.013	-12.870	1.00	23.69	1019	C	THR	A	248	54.584	-1.971	-18.736	1.00	22.17
967	CA	PHE	A	242	44.060	-11.655	-13.229	1.00	22.06	1020	O	THR	A	248	54.054	-4.349	-19.443	1.00	22.17
968	C	PHE	A	242	45.557	-11.465	-12.984	1.00	22.71	1021	CB	THR	A	248	55.680	-5.326	-18.855	1.00	17.24
969	O	PHE	A	242	46.093	-11.901	-11.969	1.00	22.30	1022	OG1	THR	A	248	54.807	-5.005	-19.903	1.00	21.11
970	CB	PHE	A	242	43.275	-10.648	-12.369	1.00	22.34	1023	CG2	THR	A	248	56.993	-2.889	-16.740	1.00	22.61
971	CG1	PHE	A	242	41.777	-10.695	-12.505	1.00	22.23	1024	N	ASN	A	249	54.184	-2.889	-16.740	1.00	22.91
972	CD1	PHE	A	242	41.137	-9.866	-13.423	1.00	21.94	1025	CA	ASN	A	249	54.530	-0.393	-14.245	1.00	24.53
973	CD2	PHE	A	242	40.996	-11.545	-11.747	1.00	22.13	1026	C	ASN	A	249	51.737	-3.081	-17.080	1.00	20.56
974	CE1	PHE	A	242	39.763	-9.870	-13.559	1.00	21.82	1027	O	ASN	A	249	50.625	-2.569	-16.955	1.00	20.56
975	CE2	PHE	A	242	39.622	-11.580	-11.923	1.00	21.18	1028	CB	ASN	A	249	52.698	-0.900	-16.304	1.00	22.75
976	CZ	PHE	A	242	38.986	-10.744	-12.823	1.00	21.58	1029	CG	ASN	A	249	53.754	-0.182	-15.455	1.00	25.70
977	N	THR	A	243	46.285	-10.845	-13.922	1.00	20.68	1030	OD1	ASN	A	249	53.878	-0.393	-14.245	1.00	24.53
978	CA	THR	A	243	47.718	-10.737	-13.888	1.00	21.11	1031	ND2	ASN	A	249	54.530	-0.640	-16.173	1.00	24.05
979	C	THR	A	243	48.264	-9.334	-14.094	1.00	21.20	1032	N	GLN	A	250	51.886	-4.178	-17.756	1.00	22.09
980	O	THR	A	243	47.787	-8.652	-14.989	1.00	19.64	1033	CA	GLN	A	250	50.791	-4.759	-18.599	1.00	21.69
981	CB	THR	A	243	48.327	-11.664	-14.974	1.00	22.96	1034	C	GLN	A	250	50.623	-5.589	-17.734	1.00	22.85
982	OG1	THR	A	243	47.919	-13.047	-14.785	1.00	24.34	1035	O	GLN	A	250	51.375	-6.152	-16.701	1.00	20.61
983	CG2	THR	A	243	49.846	-11.654	-14.938	1.00	23.70	1036	CB	GLN	A	250	52.265	-4.859	-20.720	1.00	23.80
984	N	TYR	A	244	49.357	-8.991	-13.418	1.00	21.69	1037	CG	GLN	A	250	51.509	-3.725	-21.387	1.00	25.16
985	CA	TYR	A	244	50.053	-7.712	-13.568	1.00	22.75	1038	OD1	GLN	A	250	50.566	-3.959	-22.167	1.00	24.30
986	C	TYR	A	244	51.558	-7.971	-13.653	1.00	22.82	1039	OE1	GLN	A	250	51.806	-2.490	-18.077	1.00	25.44
987	O	TYR	A	244	52.094	-8.753	-12.862	1.00	23.86	1040	NE2	GLN	A	250	48.526	-5.568	-18.077	1.00	21.86
988	CB	TYR	A	244	49.763	-6.781	-12.377	1.00	22.63	1041	N	VAL	A	251	47.558	-6.304	-17.262	1.00	21.68
989	CG	TYR	A	244	50.523	-5.466	-12.369	1.00	22.04	1042	CA	VAL	A	251	46.690	-7.203	-18.149	1.00	21.54
990	CD1	TYR	A	244	50.308	-4.453	-13.300	1.00	20.84	1043	C	VAL	A	251	46.351	-6.836	-19.273	1.00	19.04
991	CD2	TYR	A	244	51.477	-5.248	-11.386	1.00	22.48	1044	O	VAL	A	251	46.351	-6.836	-19.273	1.00	19.04
992	CE1	TYR	A	244	51.053	-3.287	-13.268	1.00	21.71	1045	CB	VAL	A	251	46.680	-5.498	-16.291	1.00	23.56
993	CE2	TYR	A	244	52.175	-4.046	-11.292	1.00	22.10	1046	CG1	VAL	A	251	47.093	-4.1039	-16.093	1.00	22.08
994	CZ	TYR	A	244	51.961	-3.071	-12.249	1.00	21.72	1047	CG2	VAL	A	251	45.175	-5.587	-16.451	1.00	22.66
995	OG	TYR	A	244	52.682	-1.888	-12.195	1.00	21.67	1048	N	PHE	A	252	46.486	-8.436	-17.687	1.00	20.51
996	N	ILE	A	245	52.258	-7.381	-14.614	1.00	21.91	1049	CA	PHE	A	252	45.764	-9.449	-18.458	1.00	21.29
997	CA	ILE	A	245	53.672	-7.500	-14.845	1.00	21.21	1050	C	PHE	A	252	44.747	-10.183	-17.592	1.00	22.46
998	C	ILE	A	245	54.362	-6.151	-14.564	1.00	22.31	1051	O	PHE	A	252	44.936	-10.267	-16.368	1.00	24.63
999	O	ILE	A	245	54.133	-5.163	-15.266	1.00	20.02	1052	CB	PHE	A	252	46.763	-10.520	-18.984	1.00	18.87
1000	CB	ILE	A	245	53.947	-7.953	-16.298	1.00	22.59	1053	CG	PHE	A	252	47.927	-9.918	-19.740	1.00	19.77
1001	CG1	ILE	A	245	53.225	-9.298	-16.560	1.00	23.96	1054	CD1	PHE	A	252	47.771	-9.602	-21.089	1.00	19.15

1055	CD2	PHE	A	252	49.087	-9.536	-19.076	1.00	19.82	1108	O	ASN	A	259	48.451	-16.546	-20.208	1.00	26.02
1056	CE1	PHE	A	252	48.807	-9.007	-21.784	1.00	18.25	1109	CB	ASN	A	259	48.371	-17.392	-23.103	1.00	25.42
1057	CE2	PHE	A	252	50.125	-8.926	-19.777	1.00	21.04	1110	CG	ASN	A	259	49.814	-17.787	-23.316	1.00	25.25
1058	CZ	PHE	A	252	49.981	-8.666	-21.127	1.00	19.76	1111	OD1	ASN	A	259	50.440	-17.469	-24.364	1.00	28.24
1059	N	ASN	A	253	43.766	-10.823	-18.207	1.00	21.21	1112	ND2	ASN	A	259	50.464	-18.457	-22.388	1.00	23.35
1060	CA	ASP	A	253	42.883	-11.739	-17.490	1.00	21.71	1113	N	GLN	A	260	48.760	-18.771	-19.919	1.00	25.82
1061	C	ASP	A	253	42.766	-13.015	-18.357	1.00	23.08	1114	CA	GLN	A	260	49.491	-18.660	-18.660	1.00	24.61
1062	O	ASP	A	253	42.922	-12.971	-19.582	1.00	20.43	1115	C	GLN	A	260	50.983	-18.858	-18.828	1.00	25.53
1063	CB	ASP	A	253	41.525	-11.192	-17.091	1.00	22.08	1116	O	GLN	A	260	51.682	-18.938	-17.782	1.00	26.85
1064	CB	ASP	A	253	40.668	-10.833	-18.296	1.00	23.51	1117	CB	GLN	A	260	48.992	-19.714	-17.639	1.00	22.83
1065	OD1	ASP	A	253	40.153	-11.833	-18.864	1.00	23.59	1118	CG	GLN	A	260	47.560	-19.480	-17.212	1.00	23.92
1066	OD2	ASP	A	253	40.550	-9.643	-18.650	1.00	22.42	1119	CD	GLN	A	260	47.324	-18.192	-16.433	1.00	24.42
1067	N	SER	A	254	42.493	-14.153	-17.717	1.00	21.89	1120	OE1	GLN	A	260	47.977	-17.871	-15.455	1.00	22.77
1068	CA	SER	A	254	42.414	-15.435	-18.370	1.00	23.57	1121	NE2	GLN	A	260	46.320	-17.451	-16.908	1.00	24.04
1069	C	SER	A	254	41.210	-15.586	-19.294	1.00	25.86	1122	N	ALA	A	261	51.524	-18.902	-20.070	1.00	24.54
1070	O	SER	A	254	41.180	-16.566	-20.049	1.00	25.58	1123	CA	ALA	A	261	52.993	-19.039	-20.165	1.00	24.10
1071	CB	SER	A	254	42.435	-16.597	-17.360	1.00	23.34	1124	C	ALA	A	261	53.724	-17.709	-19.962	1.00	23.98
1072	OG	SER	A	254	41.247	-16.555	-16.579	1.00	24.91	1125	O	ALA	A	261	54.494	-17.243	-20.832	1.00	22.89
1073	N	VAL	A	255	40.213	-14.721	-19.243	1.00	26.09	1126	CB	ALA	A	261	53.400	-19.687	-21.497	1.00	22.32
1074	CA	VAL	A	255	39.076	-14.799	-20.148	1.00	28.53	1127	N	PHE	A	262	53.543	-17.054	-18.836	1.00	24.03
1075	C	VAL	A	255	39.390	-14.071	-21.453	1.00	27.79	1128	CA	PHE	A	262	54.150	-15.787	-18.465	1.00	25.13
1076	O	VAL	A	255	39.341	-14.648	-22.555	1.00	26.52	1129	C	PHE	A	262	55.652	-15.897	-18.208	1.00	23.35
1077	CB	VAL	A	255	37.816	-14.186	-19.501	1.00	30.76	1130	O	PHE	A	262	56.198	-16.920	-17.778	1.00	22.37
1078	CG1	VAL	A	255	36.638	-14.033	-20.441	1.00	31.26	1131	CB	PHE	A	262	53.411	-15.253	-17.213	1.00	22.59
1079	CG2	VAL	A	255	37.385	-14.972	-18.275	1.00	31.36	1132	CG	PHE	A	262	52.022	-14.753	-17.488	1.00	22.84
1080	N	ASN	A	256	39.792	-12.806	-21.335	1.00	25.55	1133	CD1	PHE	A	262	50.911	-15.437	-17.022	1.00	22.43
1081	CA	ASN	A	256	40.178	-12.043	-22.536	1.00	25.41	1134	CD2	PHE	A	262	51.816	-13.575	-18.202	1.00	22.43
1082	C	ASN	A	256	41.509	-12.509	-23.144	1.00	27.70	1135	CE1	PHE	A	262	49.624	-14.989	-17.269	1.00	21.45
1083	O	ASN	A	256	41.629	-12.355	-24.377	1.00	26.77	1136	CE2	PHE	A	262	50.541	-13.133	-18.472	1.00	22.97
1084	CB	ASN	A	256	40.271	-10.550	-22.245	1.00	24.63	1137	CZ	PHE	A	262	49.440	-13.813	-18.003	1.00	22.36
1085	CG	ASN	A	256	38.942	-9.900	-21.914	1.00	24.57	1138	N	PRO	A	263	56.379	-14.800	-18.443	1.00	25.77
1086	OD1	ASN	A	256	38.017	-9.952	-22.712	1.00	24.02	1139	CA	PRO	A	263	57.810	-14.746	-18.276	1.00	27.78
1087	ND2	ASN	A	256	38.809	-9.279	-20.740	1.00	26.72	1140	C	PRO	A	263	58.230	-14.812	-16.809	1.00	29.38
1088	N	HIS	A	257	42.432	-13.073	-22.365	1.00	25.02	1141	O	PRO	A	263	57.444	-14.598	-15.893	1.00	26.79
1089	CA	HIS	A	257	43.727	-13.532	-22.914	1.00	26.70	1142	CB	PRO	A	263	58.220	-13.454	-18.976	1.00	27.35
1090	C	HIS	A	257	44.127	-14.879	-22.303	1.00	25.24	1143	CG	PRO	A	263	57.026	-12.629	-19.136	1.00	25.87
1091	O	HIS	A	257	44.864	-14.982	-21.322	1.00	22.57	1144	CD	PRO	A	263	55.836	-13.514	-18.913	1.00	27.36
1092	CB	HIS	A	257	44.801	-12.505	-22.514	1.00	27.64	1145	N	THR	A	264	59.466	-15.244	-16.602	1.00	31.59
1093	CG	HIS	A	257	46.027	-12.421	-23.350	1.00	31.69	1146	CA	THR	A	264	60.041	-15.460	-15.284	1.00	34.76
1094	ND1	HIS	A	257	46.809	-13.517	-23.674	1.00	33.57	1147	C	THR	A	264	61.224	-14.566	-14.986	1.00	35.79
1095	CD2	HIS	A	257	46.623	-11.354	-23.934	1.00	31.77	1148	O	THR	A	264	61.745	-14.682	-13.867	1.00	37.84
1096	CE1	HIS	A	257	47.830	-13.122	-24.433	1.00	34.40	1149	CB	THR	A	264	60.547	-16.920	-15.177	1.00	35.70
1097	NE2	HIS	A	257	47.743	-11.807	-24.598	1.00	34.33	1150	OG1	THR	A	264	61.354	-17.199	-16.330	1.00	37.91
1098	N	PRO	A	258	43.641	-15.986	-22.850	1.00	26.17	1151	CG2	THR	A	264	59.441	-17.952	-15.205	1.00	36.80
1099	CA	PRO	A	258	43.867	-17.303	-22.260	1.00	26.23	1152	N	SER	A	265	61.739	-13.812	-15.944	1.00	35.41
1100	C	PRO	A	258	45.227	-17.896	-22.590	1.00	26.44	1153	CA	SER	A	265	62.935	-13.002	-15.805	1.00	36.21
1101	O	PRO	A	258	45.420	-18.723	-23.495	1.00	24.80	1154	C	SER	A	265	62.656	-11.549	-15.439	1.00	37.19
1102	CB	PRO	A	258	42.694	-18.124	-22.806	1.00	27.73	1155	O	SER	A	265	61.609	-10.978	-15.750	1.00	38.21
1103	CG	PRO	A	258	42.303	-17.456	-24.089	1.00	27.71	1156	CB	SER	A	265	63.740	-13.074	-17.100	1.00	36.57
1104	CD	PRO	A	258	42.602	-15.992	-23.915	1.00	25.96	1157	OG	SER	A	265	64.697	-12.050	-17.291	1.00	35.80
1105	N	ASN	A	259	46.254	-17.533	-21.821	1.00	26.95	1158	N	SER	A	266	63.601	-10.915	-14.750	1.00	35.57
1106	CA	ASN	A	259	47.623	-18.021	-21.925	1.00	25.18	1159	CA	SER	A	266	63.488	-9.539	-14.271	1.00	34.73
1107	C	ASN	A	259	48.347	-17.710	-20.611	1.00	25.96	1160	C	SER	A	266	64.355	-8.615	-15.113	1.00	35.65

1161	O	SER A 266	64.631	-7.441	-14.841	1.00	33.89	1214	C	VAL A 274	68.515	-7.184	-4.379	1.00	26.04
1162	CB	SER A 266	63.830	-9.438	-12.779	1.00	33.46	1215	O	VAL A 274	69.229	-7.097	-3.381	1.00	26.70
1163	OG	SER A 266	62.821	-10.053	-11.983	1.00	33.15	1216	CB	VAL A 274	69.583	-6.171	-6.361	1.00	25.86
1164	N	ALA A 267	64.865	-9.185	-16.221	1.00	36.92	1217	CG1	VAL A 274	69.620	-5.082	-7.432	1.00	25.76
1165	CA	ALA A 267	65.657	-8.374	-17.145	1.00	38.86	1218	CG2	VAL A 274	70.921	-6.116	-5.640	1.00	26.10
1166	C	ALA A 267	64.766	-7.194	-17.577	1.00	40.22	1219	N	GLN A 275	67.836	-8.261	-4.692	1.00	25.69
1167	O	ALA A 267	63.560	-7.315	-17.771	1.00	38.69	1220	CA	GLN A 275	67.948	-9.534	-4.016	1.00	27.38
1168	CB	ALA A 267	66.132	-9.162	-18.339	1.00	39.06	1221	C	GLN A 275	68.722	-10.509	-4.924	1.00	26.18
1169	N	GLY A 268	65.403	-6.030	-17.573	1.00	42.28	1222	O	GLN A 275	68.335	-10.671	-6.064	1.00	24.99
1170	CA	GLY A 268	64.752	-4.784	-17.865	1.00	44.37	1223	CB	GLN A 275	66.596	-10.143	-3.662	1.00	26.97
1171	C	GLY A 268	64.348	-3.978	-16.643	1.00	46.77	1224	CG	GLN A 275	66.671	-11.477	-2.930	1.00	28.59
1172	O	GLY A 268	64.299	-2.737	-16.795	1.00	47.62	1225	CG	GLN A 275	65.265	-11.964	-2.607	1.00	32.32
1173	N	VAL A 269	64.052	-4.595	-15.480	1.00	46.24	1226	OE1	GLN A 275	64.501	-11.303	-1.895	1.00	33.16
1174	CA	VAL A 269	63.594	-3.736	-14.385	1.00	45.82	1227	NE2	GLN A 275	64.893	-13.118	-3.136	1.00	32.96
1175	C	VAL A 269	64.666	-2.835	-13.801	1.00	44.79	1228	N	LEU A 276	69.837	-11.012	-4.427	1.00	25.42
1176	O	VAL A 269	65.871	-3.071	-13.802	1.00	44.61	1229	CA	LEU A 276	70.697	-11.944	-5.130	1.00	25.50
1177	CB	VAL A 269	62.762	-4.389	-13.300	1.00	47.26	1230	C	LEU A 276	70.562	-13.358	-4.573	1.00	26.02
1178	CG1	VAL A 269	61.276	-4.187	-13.663	1.00	47.77	1231	O	LEU A 276	70.448	-13.432	-3.342	1.00	26.72
1179	CG2	VAL A 269	62.947	-5.864	-13.074	1.00	47.82	1232	CB	LEU A 276	72.157	-11.498	-5.051	1.00	23.09
1180	N	GIN A 270	64.168	-1.666	-13.364	1.00	44.38	1233	CG	LEU A 276	72.473	-10.046	-5.406	1.00	24.38
1181	CA	GIN A 270	65.117	-0.651	-12.866	1.00	43.41	1234	CD1	LEU A 276	73.930	-9.640	-5.129	1.00	23.10
1182	C	GIN A 270	65.016	-0.541	-11.348	1.00	39.99	1235	CD2	LEU A 276	72.173	-9.799	-6.886	1.00	22.76
1183	O	GIN A 270	63.909	-0.536	-10.823	1.00	39.03	1236	N	THR A 277	70.615	-14.370	-5.434	1.00	25.00
1184	CB	GIN A 270	64.909	0.628	-13.663	1.00	44.70	1237	CA	THR A 277	70.574	-15.758	-5.009	1.00	24.89
1185	CG	GIN A 270	63.545	1.259	-13.564	1.00	46.40	1238	C	THR A 277	71.967	-16.301	-5.329	1.00	25.72
1186	CD	GIN A 270	63.594	2.718	-14.049	1.00	48.21	1239	O	THR A 277	72.476	-15.942	-6.401	1.00	26.30
1187	OE1	GIN A 270	63.352	3.648	-13.263	1.00	49.65	1240	CB	THR A 277	69.479	-16.586	-5.694	1.00	27.01
1188	NE2	GIN A 270	63.949	2.916	-15.320	1.00	47.11	1241	OG1	THR A 277	68.199	-15.975	-5.436	1.00	27.31
1189	N	THR A 271	66.168	-0.620	-10.661	1.00	36.93	1242	CG2	THR A 277	69.423	-18.028	-5.179	1.00	25.75
1190	CA	THR A 271	66.136	-0.641	-9.198	1.00	32.17	1243	N	LEU A 278	72.567	-17.086	-4.445	1.00	24.33
1191	C	THR A 271	67.457	-0.271	-8.565	1.00	31.16	1244	CA	LEU A 278	73.924	-17.581	-4.635	1.00	24.69
1192	O	THR A 271	68.558	-0.403	-9.078	1.00	29.69	1245	C	LEU A 278	73.883	-19.074	-4.953	1.00	25.40
1193	CB	THR A 271	65.681	-2.033	-8.683	1.00	32.24	1246	O	LEU A 278	72.925	-19.707	-4.513	1.00	25.92
1194	CG1	THR A 271	65.608	-2.075	-7.243	1.00	30.97	1247	CB	LEU A 278	74.755	-17.375	-3.349	1.00	24.44
1195	CG2	THR A 271	66.584	-3.179	-9.133	1.00	30.31	1248	CG	LEU A 278	74.785	-15.959	-2.779	1.00	25.93
1196	N	ASN A 272	67.330	0.245	-7.332	1.00	28.98	1249	CD1	LEU A 278	75.676	-15.830	-1.528	1.00	25.09
1197	CA	ASN A 272	68.481	0.558	-6.529	1.00	26.71	1250	CD2	LEU A 278	75.228	-14.960	-3.842	1.00	25.13
1198	C	ASN A 272	68.527	-0.399	-5.322	1.00	24.87	1251	N	ALA A 279	74.866	-19.602	-5.666	1.00	25.25
1199	O	ASN A 272	69.417	-0.272	-4.515	1.00	22.11	1252	CA	ALA A 279	74.847	-21.038	-5.956	1.00	27.68
1200	CB	ASN A 272	68.464	2.031	-6.162	1.00	27.42	1253	C	ALA A 279	75.156	-21.861	-4.701	1.00	26.75
1201	CG	ASN A 272	67.423	2.457	-5.152	1.00	27.32	1254	O	ALA A 279	74.770	-23.030	-4.671	1.00	25.73
1202	OD1	ASN A 272	67.473	3.640	-4.735	1.00	28.32	1255	CB	ALA A 279	75.804	-21.373	-7.095	1.00	27.60
1203	ND2	ASN A 272	66.516	1.631	-4.751	1.00	25.56	1256	N	SER A 280	75.918	-21.347	-3.736	1.00	26.02
1204	N	LEU A 273	67.770	-1.488	-5.320	1.00	24.32	1257	CA	SER A 280	76.117	-22.146	-2.509	1.00	28.04
1205	CA	LEU A 273	67.740	-2.431	-4.206	1.00	24.89	1258	C	SER A 280	76.067	-21.219	-1.293	1.00	27.40
1206	C	LEU A 273	67.477	-3.819	-4.758	1.00	24.94	1259	O	SER A 280	76.144	-19.994	-1.449	1.00	27.94
1207	O	LEU A 273	66.401	-4.035	-5.327	1.00	23.57	1260	CB	SER A 280	77.417	-22.948	-2.579	1.00	27.93
1208	CB	LEU A 273	66.640	-2.010	-3.197	1.00	25.97	1261	CG	SER A 280	78.501	-22.049	-2.693	1.00	27.71
1209	CG	LEU A 273	66.566	-2.816	-1.893	1.00	24.77	1262	N	ALA A 281	75.919	-21.724	-0.101	1.00	26.67
1210	CD1	LEU A 273	67.763	-2.539	-0.981	1.00	23.86	1263	CA	ALA A 281	75.824	-20.907	1.108	1.00	26.36
1211	CD2	LEU A 273	65.279	-2.514	-1.136	1.00	25.15	1264	C	ALA A 281	77.169	-20.545	1.709	1.00	26.18
1212	N	VAL A 274	68.455	-4.706	-4.675	1.00	24.94	1265	O	ALA A 281	77.935	-21.377	2.183	1.00	25.41
1213	CA	VAL A 274	68.417	-5.999	-5.341	1.00	26.05	1266	CB	ALA A 281	75.004	-21.695	2.132	1.00	26.66

1267	N	PRO A 282	77.452	-19.248	1.797	1.00	27.13	1320	CD1 LEU A 288	79.857	-14.127	3.887	1.00	26.43
1268	CA	PRO A 282	78.677	-18.742	2.392	1.00	27.03	1321	CD2 LEU A 288	81.787	-15.040	2.602	1.00	24.91
1269	C	PRO A 282	78.792	-19.115	3.866	1.00	26.41	1322	N ASP A 289	82.547	-10.452	0.170	1.00	26.00
1270	O	PRO A 282	77.776	-19.312	4.518	1.00	24.07	1323	CA ASP A 289	82.295	-9.192	-0.541	1.00	28.88
1271	CB	PRO A 282	78.587	-17.226	2.229	1.00	26.75	1324	C ASP A 289	81.371	-9.408	-1.731	1.00	26.48
1272	CG	PRO A 282	77.126	-16.962	2.093	1.00	28.81	1325	O ASP A 289	81.368	-10.484	-2.310	1.00	26.03
1273	CD	PRO A 282	76.589	-18.131	1.316	1.00	27.00	1326	CB ASP A 289	83.633	-8.584	-0.985	1.00	33.27
1274	N	ASP A 283	80.031	-19.217	4.332	1.00	24.52	1327	CG ASP A 289	84.133	-7.466	-0.104	1.00	36.80
1275	CA	ASP A 283	80.333	-19.422	5.754	1.00	24.81	1328	OD1 ASP A 289	83.765	-7.242	1.063	1.00	38.78
1276	C	ASP A 283	80.147	-18.073	6.436	1.00	22.38	1329	OD2 ASP A 289	84.979	-6.701	-0.626	1.00	40.62
1277	O	ASP A 283	80.864	-17.107	6.145	1.00	21.69	1330	N VAL A 290	80.617	-8.385	-2.091	1.00	25.24
1278	CB	ASP A 283	81.775	-19.935	5.887	1.00	25.32	1331	CA VAL A 290	79.774	-8.372	-3.271	1.00	25.70
1279	CG	ASP A 283	82.210	-20.254	7.297	1.00	25.30	1332	C VAL A 290	80.162	-7.119	-4.085	1.00	27.14
1280	OD1	ASP A 283	82.960	-21.237	7.484	1.00	25.14	1333	O VAL A 290	80.498	-6.084	-3.527	1.00	26.07
1281	OD2	ASP A 283	81.801	-19.536	8.239	1.00	25.29	1334	CB VAL A 290	78.259	-8.332	-2.999	1.00	24.55
1282	N	VAL A 284	79.206	-17.940	7.380	1.00	22.67	1335	CG1 VAL A 290	77.827	-7.147	-2.128	1.00	22.41
1283	CA	VAL A 284	78.952	-16.654	8.035	1.00	22.22	1336	CG2 VAL A 290	77.423	-8.332	-4.289	1.00	23.49
1284	C	VAL A 284	80.074	-16.100	8.887	1.00	24.45	1337	N ALA A 291	80.104	-7.252	-5.408	1.00	29.18
1285	O	VAL A 284	80.021	-14.907	9.268	1.00	24.83	1338	CA ALA A 291	80.361	-6.141	-6.312	1.00	30.04
1286	CB	VAL A 284	77.642	-16.672	8.867	1.00	22.56	1339	C ALA A 291	79.519	-6.327	-7.579	1.00	30.92
1287	CG1	VAL A 284	76.463	-17.083	7.976	1.00	19.20	1340	O ALA A 291	78.916	-7.386	-7.813	1.00	29.72
1288	CG2	VAL A 284	77.712	-17.517	10.125	1.00	19.74	1341	CB ALA A 291	81.857	-6.093	-6.675	1.00	29.98
1289	N	THR A 285	81.154	-16.864	9.118	1.00	22.48	1342	N ALA A 292	79.485	-5.297	-8.406	1.00	33.04
1290	CA	THR A 285	82.292	-16.304	9.840	1.00	22.76	1343	CA ALA A 292	78.809	-5.359	-9.703	1.00	34.88
1291	C	THR A 285	83.379	-15.770	8.912	1.00	22.60	1344	C ALA A 292	79.590	-4.565	-10.738	1.00	36.66
1292	O	THR A 285	84.414	-15.336	9.433	1.00	23.50	1345	O ALA A 292	80.342	-3.645	-10.375	1.00	36.13
1293	CB	THR A 285	82.906	-17.394	10.742	1.00	22.05	1346	CB ALA A 292	77.395	-4.832	-9.570	1.00	35.02
1294	CG1	THR A 285	83.613	-18.376	9.942	1.00	22.05	1347	N ASP A 293	79.430	-4.891	-12.019	1.00	39.96
1295	CG2	THR A 285	81.829	-18.132	11.529	1.00	19.25	1348	CA ASP A 293	80.165	-4.141	-13.054	1.00	42.63
1296	N	HIS A 286	83.257	-15.892	7.608	1.00	23.16	1349	C ASP A 293	79.890	-2.644	-12.977	1.00	41.11
1297	CA	HIS A 286	84.273	-15.462	6.656	1.00	24.10	1350	O ASP A 293	78.750	-2.184	-13.100	1.00	41.97
1298	C	HIS A 286	84.119	-14.015	6.202	1.00	23.79	1351	CB ASP A 293	79.817	-4.670	-14.451	1.00	46.42
1299	O	HIS A 286	83.119	-13.382	6.557	1.00	20.85	1352	CG ASP A 293	80.532	-3.867	-15.535	1.00	49.75
1300	CB	HIS A 286	84.336	-16.407	5.450	1.00	25.64	1353	OD1 ASP A 293	81.775	-3.978	-15.683	1.00	50.50
1301	CG	HIS A 286	85.025	-17.700	5.781	1.00	26.97	1354	OD2 ASP A 293	79.821	-3.106	-16.246	1.00	51.35
1302	ND1	HIS A 286	85.197	-18.702	4.857	1.00	27.65	1355	N GLY A 294	80.904	-1.835	-12.717	1.00	40.88
1303	CD2	HIS A 286	85.496	-18.195	6.960	1.00	27.96	1356	CA GLY A 294	80.737	-0.390	-12.588	1.00	41.91
1304	CE1	HIS A 286	85.827	-19.731	5.390	1.00	27.73	1357	C GLY A 294	80.525	0.114	-11.170	1.00	41.98
1305	NE2	HIS A 286	86.003	-19.451	6.664	1.00	29.50	1358	O GLY A 294	80.616	1.353	-10.921	1.00	42.78
1306	N	ASN A 287	85.074	-13.467	5.472	1.00	23.23	1359	N TYR A 295	80.314	-0.798	-10.204	1.00	39.89
1307	CA	ASN A 287	85.032	-12.068	5.021	1.00	26.78	1360	CA TYR A 295	80.112	-0.393	-8.813	1.00	38.42
1308	C	ASN A 287	84.421	-12.025	3.625	1.00	26.70	1361	C TYR A 295	81.240	-0.871	-7.900	1.00	37.45
1309	O	ASN A 287	85.103	-12.453	2.685	1.00	26.28	1362	O TYR A 295	81.573	-2.057	-7.972	1.00	38.33
1310	CB	ASN A 287	86.459	-11.491	4.965	1.00	29.01	1363	CB TYR A 295	78.808	-0.951	-8.238	1.00	36.42
1311	CG	ASN A 287	86.508	-10.068	4.447	1.00	30.90	1364	CG TYR A 295	77.510	-0.422	-8.776	1.00	35.08
1312	OD1	ASN A 287	85.558	-9.293	4.551	1.00	31.63	1365	CD1 TYR A 295	76.787	0.576	-8.131	1.00	33.65
1313	ND2	ASN A 287	87.625	-9.643	3.861	1.00	32.44	1366	CD2 TYR A 295	77.014	-0.921	-9.988	1.00	34.53
1314	N	LEU A 288	83.160	-11.657	3.461	1.00	25.67	1367	CE1 TYR A 295	75.587	1.055	-8.644	1.00	32.54
1315	CA	LEU A 288	82.489	-11.815	2.175	1.00	25.40	1368	CE2 TYR A 295	75.851	-0.409	-10.548	1.00	33.98
1316	C	LEU A 288	82.186	-10.519	1.449	1.00	26.53	1369	CH TYR A 295	75.142	0.565	-9.856	1.00	33.30
1317	O	LEU A 288	81.557	-9.651	2.046	1.00	26.44	1370	OZ TYR A 295	73.963	1.007	-10.411	1.00	31.85
1318	CB	LEU A 288	81.178	-12.587	2.402	1.00	24.27	1371	N LYS A 296	81.795	-0.014	-7.051	1.00	36.68
1319	CG	LEU A 288	81.251	-13.809	3.317	1.00	24.57	1372	CA LYS A 296	82.757	-0.537	-6.079	1.00	36.58

1373	C	LYS A 296	82.057	-1.439	-5.060	1.00	34.22	1426	N	ARG A 303	72.765	-11.115	8.636	1.00	14.90
1374	O	LYS A 296	80.894	-1.258	-4.694	1.00	31.79	1427	CA	ARG A 303	71.700	-10.524	9.441	1.00	14.86
1375	CB	LYS A 296	83.624	0.497	-5.430	1.00	39.77	1428	C	ARG A 303	70.536	-11.502	9.653	1.00	12.98
1376	CG	LYS A 296	83.045	1.710	-4.813	1.00	43.12	1429	O	ARG A 303	70.394	-12.126	10.696	1.00	12.86
1377	CD	LYS A 296	82.983	1.676	-3.283	1.00	45.75	1430	CB	ARG A 303	71.204	-9.270	8.718	1.00	15.19
1378	CE	LYS A 296	84.388	1.604	-2.699	1.00	47.63	1431	CG	ARG A 303	69.950	-8.675	9.361	1.00	15.51
1379	NZ	LYS A 296	84.818	0.148	-2.669	1.00	48.54	1432	CD	ARG A 303	69.519	-7.377	8.675	1.00	16.61
1380	N	ALA A 297	82.840	-2.431	-4.652	1.00	30.70	1433	NE	ARG A 303	68.772	-7.664	7.445	1.00	17.37
1381	CA	ALA A 297	82.424	-3.491	-3.761	1.00	28.61	1434	CZ	ARG A 303	67.916	-6.721	7.011	1.00	19.59
1382	C	ALA A 297	82.078	-3.124	-2.319	1.00	28.36	1435	NH1	ARG A 303	67.775	-5.593	7.686	1.00	18.10
1383	O	ALA A 297	82.475	-2.094	-1.762	1.00	24.23	1436	NH2	ARG A 303	67.226	-6.920	5.887	1.00	17.39
1384	CB	ALA A 297	83.576	-4.498	-3.796	1.00	28.17	1437	N	ASN A 304	69.665	-11.600	8.626	1.00	14.70
1385	N	HIS A 298	81.359	-4.049	-1.654	1.00	25.58	1438	CA	ASN A 304	68.496	-12.476	8.741	1.00	14.47
1386	CA	HIS A 298	81.044	-3.900	-0.241	1.00	25.55	1439	C	ASN A 304	68.829	-13.961	8.551	1.00	15.73
1387	C	HIS A 298	81.031	-5.260	0.470	1.00	22.74	1440	O	ASN A 304	68.090	-14.850	8.955	1.00	16.46
1388	O	HIS A 298	80.656	-6.242	-0.135	1.00	23.46	1441	CB	ASN A 304	67.423	-12.026	7.748	1.00	14.98
1389	CB	HIS A 298	79.678	-3.242	-0.038	1.00	25.93	1442	CG	ASN A 304	66.623	-10.906	8.362	1.00	15.04
1390	CG	HIS A 298	79.409	-2.728	1.343	1.00	24.84	1443	OD1	ASN A 304	66.852	-10.495	9.494	1.00	16.92
1391	ND1	HIS A 298	79.527	-1.366	1.547	1.00	25.94	1444	ND2	ASN A 304	65.660	-10.396	7.575	1.00	14.95
1392	CD2	HIS A 298	79.039	-3.239	2.536	1.00	22.97	1445	N	VAL A 305	69.997	-14.272	8.008	1.00	15.65
1393	CB1	HIS A 298	79.249	-1.045	2.793	1.00	24.28	1446	CA	VAL A 305	70.457	-15.659	7.877	1.00	15.60
1394	NE2	HIS A 298	78.944	-2.172	3.412	1.00	23.71	1447	C	VAL A 305	70.641	-16.261	9.281	1.00	14.99
1395	N	ASN A 299	81.383	-5.265	1.739	1.00	22.36	1448	O	VAL A 305	70.346	-17.453	9.542	1.00	13.78
1396	CA	ASN A 299	81.334	-6.364	2.665	1.00	22.13	1449	CB	VAL A 305	71.763	-15.754	7.057	1.00	16.12
1397	C	ASN A 299	79.897	-6.847	2.839	1.00	20.98	1450	CG1	VAL A 305	72.886	-15.007	7.820	1.00	16.01
1398	O	ASN A 299	78.992	-6.014	2.842	1.00	17.58	1451	CG2	VAL A 305	72.211	-17.204	6.923	1.00	14.70
1399	CB	ASN A 299	81.878	-5.915	4.056	1.00	22.29	1452	N	LEU A 306	70.943	-15.455	10.302	1.00	15.35
1400	CG	ASN A 299	81.745	-7.085	5.033	1.00	22.68	1453	CA	LEU A 306	71.061	-15.925	11.682	1.00	16.85
1401	OD1	ASN A 299	82.457	-8.091	4.922	1.00	23.89	1454	C	LEU A 306	69.742	-16.291	12.359	1.00	16.79
1402	ND2	ASN A 299	80.826	-6.978	5.967	1.00	22.28	1455	O	LEU A 306	69.821	-16.866	13.444	1.00	16.11
1403	N	ILE A 300	79.663	-8.134	2.970	1.00	19.88	1456	CB	LEU A 306	71.854	-14.947	12.574	1.00	17.30
1404	CA	ILE A 300	78.342	-8.681	3.200	1.00	21.29	1457	CG	LEU A 306	73.183	-14.497	11.943	1.00	18.98
1405	C	ILE A 300	78.204	-9.065	4.694	1.00	20.22	1458	CD1	LEU A 306	73.755	-13.292	12.719	1.00	21.71
1406	O	ILE A 300	78.956	-9.925	5.183	1.00	20.11	1459	CD2	LEU A 306	74.171	-15.623	11.853	1.00	17.50
1407	CB	ILE A 300	78.053	-9.924	2.344	1.00	20.62	1460	N	ASN A 307	68.579	-16.074	11.742	1.00	17.17
1408	CG1	ILE A 300	78.330	-9.621	0.866	1.00	21.23	1461	CA	ASN A 307	67.295	-16.537	12.219	1.00	19.40
1409	CG2	ILE A 300	76.614	-10.380	2.533	1.00	21.02	1462	C	ASN A 307	67.118	-18.065	11.996	1.00	22.23
1410	CD1	ILE A 300	78.258	-10.831	-0.021	1.00	20.37	1463	O	ASN A 307	66.235	-18.629	12.645	1.00	19.61
1411	N	LEU A 301	77.336	-8.388	5.423	1.00	17.75	1464	CB	ASN A 307	66.072	-15.914	11.520	1.00	17.50
1412	CA	LEU A 301	77.209	-8.699	6.870	1.00	18.06	1465	CG	ASN A 307	65.952	-14.411	11.499	1.00	19.19
1413	C	LEU A 301	76.024	-9.630	7.119	1.00	17.18	1466	OD1	ASN A 307	66.604	-13.703	12.268	1.00	16.40
1414	O	LEU A 301	74.921	-9.397	6.603	1.00	15.63	1467	ND2	ASN A 307	65.093	-13.861	10.615	1.00	16.76
1415	CB	LEU A 301	77.007	-7.399	7.657	1.00	17.96	1468	N	LEU A 308	67.846	-18.698	11.079	1.00	20.99
1416	CG	LEU A 301	77.055	-7.516	9.198	1.00	19.15	1469	CA	LEU A 308	67.709	-20.121	10.793	1.00	20.83
1417	CD1	LEU A 301	78.494	-7.470	9.695	1.00	17.41	1470	C	LEU A 308	67.998	-21.006	11.995	1.00	21.03
1418	CD2	LEU A 301	76.236	-6.376	9.814	1.00	17.81	1471	O	LEU A 308	68.784	-20.723	12.906	1.00	18.48
1419	N	PRO A 302	76.217	-10.719	7.848	1.00	15.47	1472	CB	LEU A 308	68.641	-20.561	9.636	1.00	21.47
1420	CA	PRO A 302	75.088	-11.614	8.092	1.00	15.32	1473	CB	LEU A 308	68.405	-19.861	8.291	1.00	23.03
1421	C	PRO A 302	74.052	-10.972	9.021	1.00	15.88	1474	CD1	LEU A 308	69.489	-20.134	7.261	1.00	23.09
1422	O	PRO A 302	74.372	-10.349	10.023	1.00	16.78	1475	CD2	LEU A 308	67.039	-20.248	7.739	1.00	21.71
1423	CB	PRO A 302	75.628	-12.891	8.738	1.00	14.74	1476	N	PRO A 309	67.320	-22.166	12.049	1.00	20.22
1424	CG	PRO A 302	77.150	-12.804	8.778	1.00	16.15	1477	CA	PRO A 309	67.416	-23.095	13.161	1.00	19.80
1425	CD	PRO A 302	77.395	-11.247	8.517	1.00	15.56	1478	C	PRO A 309	68.812	-23.561	13.507	1.00	19.00

1479	O	PRO A 309	69.113	-23.663	14.715	1.00	19.17	1532	N	GLY A 315	69.182	-23.694	25.070	1.00	24.12
1480	CB	PRO A 309	66.476	-24.256	12.793	1.00	20.37	1533	CA	GLY A 315	69.527	-24.093	26.451	1.00	24.72
1481	CG	PRO A 309	65.446	-23.573	11.949	1.00	19.19	1534	C	GLY A 315	69.338	-22.967	27.451	1.00	25.47
1482	CD	PRO A 309	66.282	-22.609	11.100	1.00	19.26	1535	O	GLY A 315	69.165	-21.816	27.048	1.00	26.04
1483	N	ARG A 310	69.744	-23.653	12.564	1.00	18.57	1536	N	ASN A 316	69.339	-23.228	28.754	1.00	25.24
1484	CA	ARG A 310	71.114	-24.027	12.882	1.00	18.99	1537	CA	ASN A 316	69.116	-22.249	29.805	1.00	25.73
1485	C	ARG A 310	71.813	-23.033	13.806	1.00	20.10	1538	C	ASN A 316	70.397	-21.804	30.509	1.00	25.95
1486	O	ARG A 310	72.758	-23.400	14.544	1.00	19.39	1539	O	ASN A 316	70.298	-21.278	31.638	1.00	24.29
1487	CB	ARG A 310	71.910	-24.244	11.582	1.00	21.29	1540	CB	ASN A 316	68.190	-22.893	30.866	1.00	29.42
1488	CG	ARG A 310	72.315	-22.947	10.876	1.00	23.49	1541	CG	ASN A 316	68.861	-23.980	31.705	1.00	33.78
1489	CD	ARG A 310	73.173	-23.235	9.648	1.00	25.45	1542	OD1	ASN A 316	70.048	-24.341	31.528	1.00	33.72
1490	NE	ARG A 310	74.564	-23.436	10.024	1.00	30.55	1543	ND2	ASN A 316	68.154	-24.553	32.687	1.00	34.41
1491	CZ	ARG A 310	75.583	-23.674	9.187	1.00	33.31	1544	N	ASP A 317	71.584	-22.038	29.911	1.00	21.74
1492	NH1	ARG A 310	75.463	-23.744	7.854	1.00	33.05	1545	CA	ASP A 317	72.807	-21.719	30.606	1.00	21.65
1493	NH2	ARG A 310	76.793	-23.814	9.703	1.00	33.33	1546	C	ASP A 317	73.650	-20.592	30.037	1.00	22.99
1494	N	TYR A 311	71.378	-21.761	13.838	1.00	18.74	1547	O	ASP A 317	74.868	-20.599	30.297	1.00	22.74
1495	CA	TYR A 311	71.933	-20.818	14.800	1.00	19.14	1548	CB	ASP A 317	73.665	-23.009	30.705	1.00	22.71
1496	C	TYR A 311	71.067	-20.575	16.024	1.00	19.76	1549	CG	ASP A 317	74.073	-23.483	29.316	1.00	23.13
1497	O	TYR A 311	71.260	-19.550	16.682	1.00	19.20	1550	OD1	ASP A 317	73.271	-23.346	28.363	1.00	22.02
1498	CB	TYR A 311	72.119	-19.454	14.074	1.00	20.52	1551	OD2	ASP A 317	75.185	-24.003	29.157	1.00	22.43
1499	CG	TYR A 311	72.939	-19.630	12.795	1.00	20.06	1552	N	LEU A 318	73.097	-19.656	29.260	1.00	22.59
1500	CD1	TYR A 311	72.341	-19.445	11.558	1.00	19.78	1553	CA	LEU A 318	73.889	-18.531	28.754	1.00	20.66
1501	CD2	TYR A 311	74.254	-20.025	12.854	1.00	19.22	1554	C	LEU A 318	74.316	-17.676	29.955	1.00	20.42
1502	CE1	TYR A 311	73.093	-19.612	10.395	1.00	21.56	1555	O	LEU A 318	73.547	-17.564	30.903	1.00	17.61
1503	CE2	TYR A 311	75.018	-20.203	11.703	1.00	20.95	1556	CB	LEU A 318	73.169	-17.678	27.715	1.00	20.60
1504	CZ	TYR A 311	74.425	-19.993	10.480	1.00	21.56	1557	CG	LEU A 318	72.798	-18.391	26.385	1.00	19.68
1505	OH	TYR A 311	75.159	-20.170	9.329	1.00	24.43	1558	CD1	LEU A 318	71.963	-17.493	25.495	1.00	17.29
1506	N	ASP A 312	70.069	-21.385	16.314	1.00	22.16	1559	CD2	LEU A 318	74.109	-18.776	25.680	1.00	16.96
1507	CA	ASP A 312	69.147	-21.132	17.421	1.00	24.33	1560	N	GLY A 319	75.550	-17.187	29.890	1.00	20.73
1508	C	ASP A 312	69.426	-21.956	18.667	1.00	22.29	1561	CA	GLY A 319	76.193	-16.428	30.949	1.00	20.43
1509	O	ASP A 312	69.166	-23.155	18.676	1.00	22.82	1562	C	GLY A 319	77.202	-17.295	31.721	1.00	22.10
1510	CB	ASP A 312	67.703	-21.360	16.940	1.00	25.85	1563	O	GLY A 319	77.914	-18.124	31.117	1.00	21.40
1511	CG	ASP A 312	66.717	-20.989	18.046	1.00	30.43	1564	N	ASN A 320	77.286	-17.098	33.042	1.00	19.98
1512	OD1	ASP A 312	66.756	-19.889	18.609	1.00	30.37	1565	CA	ASN A 320	78.191	-17.952	33.835	1.00	21.91
1513	OD2	ASP A 312	65.841	-21.814	18.382	1.00	33.45	1566	C	ASN A 320	77.375	-18.729	34.867	1.00	22.53
1514	N	TYR A 313	69.905	-21.325	19.725	1.00	21.56	1567	O	ASN A 320	76.333	-18.231	35.331	1.00	21.27
1515	CA	TYR A 313	70.305	-22.052	20.933	1.00	21.31	1568	CB	ASN A 320	79.297	-17.159	34.508	1.00	21.04
1516	C	TYR A 313	69.224	-21.924	21.996	1.00	22.83	1569	CG	ASN A 320	78.807	-16.191	35.571	1.00	21.43
1517	O	TYR A 313	68.987	-20.799	22.457	1.00	20.91	1570	OD1	ASN A 320	78.574	-16.655	36.680	1.00	22.62
1518	CB	TYR A 313	71.644	-21.503	21.452	1.00	20.67	1571	ND2	ASN A 320	78.589	-14.900	35.304	1.00	18.58
1519	CG	TYR A 313	72.137	-22.255	22.674	1.00	19.10	1572	N	VAL A 321	77.797	-19.940	35.176	1.00	22.76
1520	CD1	TYR A 313	72.697	-23.521	22.532	1.00	18.67	1573	CA	VAL A 321	77.084	-20.812	36.124	1.00	22.43
1521	CD2	TYR A 313	71.998	-21.744	23.956	1.00	18.42	1574	C	VAL A 321	78.113	-21.225	37.192	1.00	24.11
1522	CE1	TYR A 313	73.148	-24.247	23.621	1.00	19.13	1575	O	VAL A 321	78.998	-22.018	36.899	1.00	23.74
1523	CE2	TYR A 313	72.416	-22.475	25.069	1.00	17.61	1576	CB	VAL A 321	76.477	-22.041	35.464	1.00	24.06
1524	CZ	TYR A 313	72.994	-23.703	24.889	1.00	19.22	1577	CG1	VAL A 321	75.861	-23.044	36.476	1.00	25.33
1525	OH	TYR A 313	73.413	-24.442	25.989	1.00	18.27	1578	CG2	VAL A 321	75.396	-21.628	34.452	1.00	23.25
1526	N	SER A 314	68.599	-23.055	22.329	1.00	23.06	1579	N	TYR A 322	78.040	-20.600	38.364	1.00	24.47
1527	CA	SER A 314	67.542	-23.000	23.332	1.00	25.19	1580	CA	TYR A 322	79.021	-20.745	39.416	1.00	26.10
1528	C	SER A 314	67.926	-23.474	24.719	1.00	25.25	1581	C	TYR A 322	78.764	-21.897	40.382	1.00	26.90
1529	O	SER A 314	67.000	-23.528	25.550	1.00	25.31	1582	O	TYR A 322	77.658	-22.184	40.816	1.00	25.89
1530	CB	SER A 314	66.307	-23.804	22.843	1.00	27.03	1583	CB	TYR A 322	79.122	-19.432	40.251	1.00	25.11
1531	OG	SER A 314	66.672	-25.175	22.739	1.00	28.18	1584	CG	TYR A 322	79.911	-19.624	41.541	1.00	25.40

1585	CD1	TYR	A	322	81.291	-19.576	41.519	1.00	25.69	1638	CD1	PHE	A	329	83.556	-19.478	32.308	1.00	16.87
1586	CD2	TYR	A	322	79.282	-19.866	42.764	1.00	25.12	1639	CD2	PHE	A	329	82.377	-17.385	32.209	1.00	19.26
1587	CE1	TYR	A	322	82.037	-19.772	42.669	1.00	26.68	1640	CE1	PHE	A	329	84.195	-19.074	33.465	1.00	19.15
1588	CE2	TYR	A	322	80.010	-20.046	43.920	1.00	26.18	1641	CE2	PHE	A	329	83.064	-16.954	33.344	1.00	18.66
1589	CZ	TYR	A	322	81.383	-19.999	43.871	1.00	26.75	1642	CZ	PHE	A	329	83.904	-17.819	33.995	1.00	19.30
1590	OH	TYR	A	322	82.145	-20.197	44.987	1.00	27.96	1643	N	ARG	A	330	79.142	-19.576	28.754	1.00	19.04
1591	N	SER	A	323	79.858	-22.517	40.812	1.00	27.80	1644	CA	ARG	A	330	78.571	-19.791	27.432	1.00	17.97
1592	CA	SER	A	323	79.884	-23.498	41.882	1.00	28.44	1645	C	ARG	A	330	78.029	-18.474	26.858	1.00	19.63
1593	O	SER	A	323	81.291	-23.469	42.494	1.00	28.56	1646	O	ARG	A	330	77.319	-17.717	27.557	1.00	18.47
1594	C	SER	A	323	82.252	-22.944	41.901	1.00	28.33	1647	CB	ARG	A	330	77.471	-20.860	27.393	1.00	20.74
1595	CB	SER	A	323	79.467	-24.897	41.536	1.00	27.55	1648	CG	ARG	A	330	77.092	-21.262	25.948	1.00	21.20
1596	CG	SER	A	323	80.342	-25.551	40.633	1.00	29.60	1649	CD	ARG	A	330	75.983	-22.295	25.893	1.00	21.96
1597	N	LYS	A	324	81.399	-24.048	43.683	1.00	29.32	1650	NE	ARG	A	330	76.296	-23.594	26.492	1.00	22.92
1598	CA	LYS	A	324	82.674	-24.064	44.394	1.00	31.61	1651	CZ	ARG	A	330	76.812	-24.638	25.839	1.00	23.47
1599	C	LYS	A	324	83.804	-24.679	43.609	1.00	30.15	1652	NH1	ARG	A	330	77.076	-25.760	26.503	1.00	23.14
1600	O	LYS	A	324	84.882	-24.101	43.574	1.00	29.36	1653	NH2	ARG	A	330	77.034	-24.625	24.528	1.00	20.70
1601	CB	LYS	A	324	82.529	-24.863	45.697	1.00	40.11	1654	N	VAL	A	331	78.431	-18.196	25.605	1.00	18.50
1602	CG	LYS	A	324	82.413	-23.989	46.937	1.00	40.11	1655	CA	VAL	A	331	77.991	-16.939	24.952	1.00	18.28
1603	CD	LYS	A	324	82.177	-24.926	48.134	1.00	42.85	1656	C	VAL	A	331	77.605	-17.227	23.505	1.00	17.02
1604	CE	LYS	A	324	80.295	-25.015	48.452	1.00	44.71	1657	O	VAL	A	331	78.271	-18.081	22.888	1.00	17.84
1605	NZ	LYS	A	324	80.523	-23.993	49.436	1.00	46.25	1658	CB	VAL	A	331	79.103	-15.885	25.030	1.00	17.74
1606	N	ASP	A	325	83.595	-25.836	42.979	1.00	30.61	1659	CG1	VAL	A	331	80.369	-16.391	24.330	1.00	18.41
1607	CA	ASP	A	325	84.674	-26.467	42.219	1.00	31.24	1660	CG2	VAL	A	331	78.693	-14.550	24.432	1.00	18.27
1608	O	ASP	A	325	84.934	-25.989	40.810	1.00	30.11	1661	N	TRP	A	332	76.561	-16.576	22.985	1.00	17.30
1609	C	ASP	A	325	86.033	-26.273	40.306	1.00	28.10	1662	CA	TRP	A	332	76.128	-16.832	21.606	1.00	16.55
1610	CB	ASP	A	325	84.435	-27.990	42.162	1.00	34.10	1663	C	TRP	A	332	76.872	-15.935	20.635	1.00	16.29
1611	CG	ASP	A	325	84.438	-28.490	43.607	1.00	38.46	1664	O	TRP	A	332	76.694	-14.711	20.747	1.00	16.81
1612	OD1	ASP	A	325	85.027	-27.884	44.523	1.00	39.44	1665	CB	TRP	A	332	74.607	-16.801	21.475	1.00	15.95
1613	OD2	ASP	A	325	83.746	-29.499	43.857	1.00	40.94	1666	CG	TRP	A	332	73.976	-17.064	20.126	1.00	16.61
1614	N	ALA	A	326	84.007	-25.274	40.168	1.00	26.93	1667	CD1	TRP	A	332	73.873	-18.291	19.532	1.00	16.92
1615	CA	ALA	A	326	84.236	-24.816	38.800	1.00	24.07	1668	CD2	TRP	A	332	73.332	-16.134	19.237	1.00	16.47
1616	C	ALA	A	326	83.169	-23.821	38.324	1.00	23.18	1669	NE1	TRP	A	332	73.231	-18.170	18.311	1.00	18.27
1617	O	ALA	A	326	82.044	-23.822	38.845	1.00	23.26	1670	CE2	TRP	A	332	72.866	-16.865	18.119	1.00	17.73
1618	CB	ALA	A	326	84.066	-26.016	37.844	1.00	25.03	1671	CE3	TRP	A	332	73.178	-14.747	19.217	1.00	16.21
1619	N	THR	A	327	83.521	-23.011	37.336	1.00	22.27	1672	CZ2	TRP	A	332	72.274	-16.256	17.010	1.00	16.41
1620	CA	THR	A	327	82.521	-22.114	36.751	1.00	22.23	1673	CZ3	TRP	A	332	72.531	-14.138	18.143	1.00	16.52
1621	C	THR	A	327	82.410	-22.371	35.241	1.00	23.00	1674	CH2	TRP	A	332	72.075	-14.905	17.057	1.00	15.60
1622	O	THR	A	327	83.464	-22.441	34.587	1.00	22.16	1675	N	ALA	A	333	77.714	-16.446	19.737	1.00	16.60
1623	CB	THR	A	327	82.822	-20.630	36.971	1.00	22.19	1676	CA	ALA	A	333	78.444	-15.553	18.786	1.00	17.33
1624	CG1	THR	A	327	82.652	-20.444	38.359	1.00	20.51	1677	C	ALA	A	333	78.657	-16.275	17.466	1.00	17.44
1625	CG2	THR	A	327	81.815	-19.716	36.226	1.00	21.57	1678	O	ALA	A	333	79.767	-16.726	17.165	1.00	17.32
1626	N	SER	A	328	81.189	-22.495	34.728	1.00	20.66	1679	CB	ALA	A	333	79.803	-15.187	19.395	1.00	16.81
1627	CA	SER	A	328	81.065	-22.697	33.273	1.00	21.04	1680	N	PRO	A	334	77.615	-16.422	16.640	1.00	16.81
1628	C	SER	A	328	80.570	-21.437	32.555	1.00	21.82	1681	CA	PRO	A	334	77.667	-17.222	15.426	1.00	16.90
1629	O	SER	A	328	79.704	-20.724	33.080	1.00	20.39	1682	C	PRO	A	334	78.499	-16.717	14.264	1.00	18.09
1630	CB	SER	A	328	80.013	-23.762	33.010	1.00	22.57	1683	O	PRO	A	334	78.812	-17.501	13.340	1.00	19.01
1631	CG	SER	A	328	80.420	-25.021	33.487	1.00	26.12	1684	CB	PRO	A	334	76.165	-17.379	15.095	1.00	17.28
1632	N	PHE	A	329	81.055	-21.187	31.335	1.00	20.94	1685	CD	PRO	A	334	75.567	-16.049	15.533	1.00	17.13
1633	CA	PHE	A	329	80.703	-19.990	30.587	1.00	19.32	1686	CG	PRO	A	334	76.259	-15.842	16.881	1.00	15.63
1634	C	PHE	A	329	80.108	-20.361	29.232	1.00	20.62	1687	N	THR	A	335	78.966	-15.478	14.258	1.00	17.49
1635	O	PHE	A	329	80.520	-21.374	28.618	1.00	18.58	1688	CA	THR	A	335	79.765	-14.969	13.145	1.00	19.36
1636	CB	PHE	A	329	81.937	-19.097	30.414	1.00	17.82	1689	C	THR	A	335	81.245	-14.804	13.484	1.00	19.67
1637	CG	PHE	A	329	82.637	-18.648	31.677	1.00	19.59	1690	O	THR	A	335	82.095	-14.363	12.681	1.00	19.24

1691	CB	THR A 335	79.202	-13.632	12.595	1.00	19.04	1744	CD2 LEU A 342	91.270	-12.283	27.239	1.00	24.22
1692	OG1	THR A 335	79.459	-12.557	13.518	1.00	18.31	1745	N LEU A 343	90.090	-13.551	32.167	1.00	21.42
1693	CG2	THR A 335	77.709	-13.744	12.268	1.00	18.55	1746	CA LEU A 343	89.834	-13.675	33.594	1.00	22.82
1694	N	ALA A 336	81.589	-15.082	14.737	1.00	20.15	1747	C LEU A 343	90.771	-12.755	34.359	1.00	23.56
1695	CA	ALA A 336	82.961	-14.943	15.225	1.00	21.16	1748	O LEU A 343	91.973	-12.618	34.049	1.00	22.34
1696	C	ALA A 336	83.915	-16.034	14.731	1.00	20.66	1749	CB LEU A 343	89.977	-15.095	34.112	1.00	23.13
1697	O	ALA A 336	83.522	-17.199	14.668	1.00	20.80	1750	CG LEU A 343	88.936	-16.134	33.765	1.00	24.04
1698	CB	ALA A 336	82.965	-15.048	16.765	1.00	19.61	1751	CD1 LEU A 343	89.386	-17.523	34.242	1.00	22.59
1699	N	SER A 337	85.164	-15.642	14.454	1.00	21.24	1752	CD2 LEU A 343	87.574	-15.819	34.402	1.00	22.28
1700	CA	SER A 337	86.158	-16.646	14.033	1.00	21.72	1753	N TYR A 344	90.187	-12.001	35.296	1.00	21.67
1701	C	SER A 337	86.913	-17.153	15.263	1.00	22.44	1754	CA TYR A 344	90.891	-11.029	36.081	1.00	20.84
1702	O	SER A 337	87.457	-18.262	15.262	1.00	22.33	1755	C TYR A 344	90.731	-11.309	37.578	1.00	22.98
1703	CB	SER A 337	87.101	-16.133	12.942	1.00	19.79	1756	O TYR A 344	89.595	-11.488	38.042	1.00	20.73
1704	OG	SER A 337	87.842	-15.014	13.378	1.00	19.73	1757	CB TYR A 344	90.471	-9.590	35.781	1.00	22.01
1705	N	ASN A 338	86.800	-16.461	16.395	1.00	22.39	1758	CG TYR A 344	90.514	-9.119	34.350	1.00	22.91
1706	CA	ASN A 338	87.474	-16.897	17.629	1.00	22.59	1759	CD1 TYR A 344	89.464	-9.443	33.473	1.00	23.47
1707	C	ASN A 338	86.895	-16.133	18.822	1.00	21.70	1760	CD2 TYR A 344	91.589	-8.413	33.839	1.00	23.31
1708	O	ASN A 338	86.551	-14.961	18.662	1.00	20.21	1761	CE1 TYR A 344	89.503	-9.068	32.134	1.00	22.88
1709	CB	ASN A 338	88.985	-16.546	17.593	1.00	23.25	1762	CE2 TYR A 344	91.600	-7.977	32.516	1.00	24.05
1710	CG	ASN A 338	89.769	-17.286	18.665	1.00	23.27	1763	CZ TYR A 344	90.574	-8.343	31.665	1.00	23.45
1711	OD1	ASN A 338	90.949	-16.819	19.176	1.00	24.41	1764	OH TYR A 344	90.607	-7.928	30.344	1.00	21.39
1712	ND2	ASN A 338	86.788	-16.750	19.982	1.00	20.64	1765	N ASN A 345	91.843	-11.311	38.344	1.00	23.99
1713	N	VAL A 339	86.296	-16.110	21.195	1.00	20.83	1766	CA ASN A 345	91.708	-11.557	39.793	1.00	26.27
1714	CA	VAL A 339	87.216	-16.633	22.325	1.00	21.76	1767	C ASN A 345	91.603	-10.255	40.558	1.00	26.36
1715	C	VAL A 339	87.446	-17.852	22.405	1.00	20.76	1768	O ASN A 345	91.850	-10.193	41.752	1.00	28.06
1716	O	VAL A 339	84.849	-16.455	21.599	1.00	20.75	1769	CB ASN A 345	92.841	-12.427	40.366	1.00	27.33
1717	CB	VAL A 339	84.446	-15.701	22.879	1.00	20.39	1770	CG ASN A 345	94.204	-11.783	40.253	1.00	27.96
1718	CG1	VAL A 339	83.840	-16.157	20.492	1.00	20.29	1771	OD1 ASN A 345	94.333	-10.580	39.995	1.00	26.96
1719	CG2	VAL A 339	87.759	-15.716	23.111	1.00	19.11	1772	ND2 ASN A 345	95.254	-12.588	40.461	1.00	30.19
1720	N	GLN A 340	88.577	-16.086	24.253	1.00	21.95	1773	N SER A 346	91.183	-9.172	39.904	1.00	27.11
1721	CA	GLN A 340	87.972	-15.504	25.543	1.00	22.76	1774	CA SER A 346	91.040	-7.885	40.569	1.00	26.45
1722	C	GLN A 340	87.332	-14.438	25.536	1.00	20.68	1775	C SER A 346	90.101	-7.018	39.745	1.00	26.06
1723	O	GLN A 340	90.005	-15.531	24.024	1.00	25.09	1776	O SER A 346	89.895	-7.299	38.564	1.00	26.29
1724	CB	GLN A 340	90.662	-16.091	22.738	1.00	28.48	1777	CB SER A 346	92.413	-7.241	40.740	1.00	24.63
1725	CG	GLN A 340	92.158	-15.840	22.679	1.00	32.41	1778	OG SER A 346	92.769	-6.551	39.569	1.00	23.97
1726	CD	GLN A 340	92.611	-14.980	21.913	1.00	34.76	1779	N GLU A 347	89.587	-5.953	40.320	1.00	25.01
1727	OE1	GLN A 340	92.927	-16.566	23.479	1.00	32.06	1780	CA GLU A 347	88.629	-5.103	39.610	1.00	26.48
1728	NE2	GLN A 340	88.203	-16.164	26.673	1.00	21.03	1781	C GLU A 347	89.285	-4.207	38.593	1.00	27.56
1729	N	LEU A 341	87.802	-15.701	27.996	1.00	19.98	1782	O GLU A 347	88.618	-3.846	37.608	1.00	26.07
1730	CA	LEU A 341	88.980	-14.997	28.691	1.00	20.18	1783	CB GLU A 347	87.833	-4.290	40.665	1.00	26.52
1731	C	LEU A 341	90.067	-15.556	28.788	1.00	18.71	1784	CG GLU A 347	86.563	-3.647	40.158	1.00	25.42
1732	O	LEU A 341	87.383	-16.917	28.829	1.00	19.90	1785	CD GLU A 347	85.681	-3.082	41.265	1.00	25.59
1733	CB	LEU A 341	86.998	-16.678	30.295	1.00	21.43	1786	OE1 GLU A 347	84.477	-2.829	41.018	1.00	23.17
1734	CG	LEU A 341	85.703	-15.837	30.345	1.00	20.84	1787	OE2 GLU A 347	86.140	-2.884	42.416	1.00	24.63
1735	CD1	LEU A 341	86.828	-18.018	31.006	1.00	20.08	1788	N LYS A 348	90.532	-3.758	38.843	1.00	27.94
1736	CD2	LEU A 341	88.796	-13.750	29.074	1.00	19.42	1789	CA LYS A 348	91.239	-2.907	37.892	1.00	30.23
1737	N	LEU A 342	89.731	-12.963	29.842	1.00	21.69	1790	C LYS A 348	92.602	-3.443	37.434	1.00	30.18
1738	CA	LEU A 342	89.252	-12.963	31.306	1.00	22.85	1791	O LYS A 348	93.183	-2.871	36.515	1.00	30.31
1739	C	LEU A 342	88.125	-12.555	31.641	1.00	21.27	1792	CB LYS A 348	91.496	-1.484	38.403	1.00	32.74
1740	O	LEU A 342	89.901	-11.557	29.277	1.00	22.45	1793	CG LYS A 348	90.350	-0.740	39.058	1.00	36.60
1741	CB	LEU A 342	90.120	-11.437	27.750	1.00	23.01	1794	CD LYS A 348	90.397	-0.890	40.579	1.00	39.69
1742	CG	LEU A 342	90.324	-9.977	27.354	1.00	20.48	1795	CE LYS A 348	91.755	-0.453	41.157	1.00	40.78
1743	CD1	LEU A 342						1796	NZ LYS A 348	91.956	-0.820	42.572	1.00	40.05



1850	C	GLU A 356	89.240	-20.795	24.749	1.00	24.21
1851	CB	GLU A 356	89.220	-21.728	25.556	1.00	24.57
1852	CB	GLU A 356	91.263	-21.110	23.354	1.00	26.34
1853	CG	GLU A 356	92.307	-20.425	22.486	1.00	28.70
1854	CD	GLU A 356	91.664	-19.583	21.391	1.00	29.91
1855	OE1	GLU A 356	90.508	-19.768	20.973	1.00	30.84
1856	OE2	GLU A 356	92.360	-18.651	20.957	1.00	31.88
1857	N	MET A 357	88.138	-20.398	24.144	1.00	24.03
1858	CA	MET A 357	86.839	-21.025	24.390	1.00	21.73
1859	C	MET A 357	86.645	-22.023	23.268	1.00	22.56
1860	CB	MET A 357	87.422	-21.932	22.306	1.00	23.10
1861	CB	MET A 357	85.724	-19.974	24.468	1.00	20.62
1862	CG	MET A 357	85.893	-19.016	25.636	1.00	19.78
1863	CD	MET A 357	84.518	-17.881	25.954	1.00	18.56
1864	CE	MET A 357	83.209	-19.002	26.424	1.00	17.50
1865	N	GLN A 358	85.749	-22.969	23.351	1.00	23.45
1866	CA	GLN A 358	85.504	-23.939	22.312	1.00	26.55
1867	C	GLN A 358	84.150	-23.684	21.603	1.00	25.08
1868	CB	GLN A 358	83.110	-23.528	22.253	1.00	21.83
1869	CG	GLN A 358	85.324	-25.373	22.847	1.00	29.06
1870	CG	GLN A 358	85.931	-25.673	24.194	1.00	36.05
1871	OE1	GLN A 358	85.318	-26.928	24.804	1.00	38.87
1872	OE1	GLN A 358	85.386	-27.019	26.035	1.00	42.36
1873	NE2	GLN A 358	84.727	-27.807	23.987	1.00	40.44
1874	N	LYS A 359	84.197	-23.798	20.304	1.00	24.04
1875	CA	LYS A 359	83.007	-23.709	19.465	1.00	26.25
1876	C	LYS A 359	82.043	-24.816	19.852	1.00	24.84
1877	C	LYS A 359	82.493	-25.956	19.974	1.00	26.51
1878	CB	LYS A 359	83.343	-23.834	17.978	1.00	26.51
1879	CG	LYS A 359	82.110	-23.602	17.112	1.00	29.91
1880	CD	LYS A 359	81.361	-22.329	17.504	1.00	30.23
1881	CE	LYS A 359	79.954	-22.267	16.933	1.00	28.64
1882	NZ	LYS A 359	80.031	-22.364	15.441	1.00	28.49
1883	N	SER A 360	80.782	-24.516	20.104	1.00	23.90
1884	CA	SER A 360	79.794	-25.489	20.549	1.00	23.71
1885	C	SER A 360	78.515	-25.385	19.738	1.00	24.86
1886	O	SER A 360	78.513	-24.861	18.608	1.00	23.35
1887	CB	SER A 360	78.641	-26.216	22.656	1.00	23.14
1888	OG	SER A 360	77.405	-25.945	20.249	1.00	22.35
1889	N	ASP A 361	76.173	-25.979	19.475	1.00	25.63
1890	CA	ASP A 361	75.582	-24.625	19.066	1.00	23.92
1891	C	ASP A 361	75.515	-23.693	19.861	1.00	21.92
1892	O	ASP A 361	75.057	-26.676	20.281	1.00	29.13
1893	CB	ASP A 361	75.440	-28.089	20.700	1.00	33.65
1894	CG	ASP A 361	76.245	-28.789	20.062	1.00	34.34
1895	OD1	ASP A 361	74.868	-28.505	21.735	1.00	37.02
1896	OD2	ASP A 361	74.897	-24.624	17.935	1.00	22.19
1897	N	ASN A 362	74.108	-23.504	17.439	1.00	20.84
1898	CA	ASN A 362	74.723	-22.135	17.566	1.00	20.78
1899	C	ASN A 362	74.034	-21.188	18.003	1.00	22.45
1900	O	ASN A 362	72.734	-23.521	18.149	1.00	21.03
1901	CB	ASN A 362	72.027	-24.871	18.007	1.00	21.03
1902	CG	ASN A 362					

1903	OD1	ASN A 362	71.503	-25.284	16.951	1.00	20.90	1956	N	VAL A 369	85.811	-23.779	33.570	1.00	25.22
1904	ND2	ASN A 362	71.904	-25.578	19.095	1.00	17.27	1957	CA	VAL A 369	87.072	-23.466	34.227	1.00	26.94
1905	N	GLY A 363	75.986	-21.960	17.142	1.00	19.74	1958	C	VAL A 369	87.104	-24.075	35.641	1.00	27.56
1906	CA	GLY A 363	76.621	-20.650	17.206	1.00	18.96	1959	O	VAL A 369	86.251	-23.711	36.453	1.00	26.74
1907	C	GLY A 363	77.260	-20.272	18.543	1.00	18.21	1960	CB	VAL A 369	87.404	-21.975	34.403	1.00	27.02
1908	O	GLY A 363	77.931	-19.229	18.591	1.00	15.89	1961	CG1	VAL A 369	88.793	-21.803	35.043	1.00	28.37
1909	N	THR A 364	77.156	-21.080	19.578	1.00	15.00	1962	CG2	VAL A 369	87.375	-21.200	33.086	1.00	26.62
1910	CA	THR A 364	77.689	-20.699	20.880	1.00	17.37	1963	N	SER A 370	88.133	-24.863	35.929	1.00	27.55
1911	C	THR A 364	79.156	-21.147	21.019	1.00	17.64	1964	CA	SER A 370	88.332	-25.436	37.261	1.00	30.11
1912	O	THR A 364	79.666	-21.891	20.195	1.00	17.37	1965	C	SER A 370	88.809	-24.485	38.333	1.00	27.75
1913	CB	THR A 364	76.957	-21.274	22.108	1.00	17.36	1966	O	SER A 370	89.579	-23.573	38.078	1.00	28.00
1914	OG1	THR A 364	76.996	-22.715	22.132	1.00	18.13	1967	CB	SER A 370	89.397	-26.574	37.177	1.00	31.50
1915	CG2	THR A 364	75.462	-20.902	22.195	1.00	18.48	1968	OG	SER A 370	88.799	-27.545	36.318	1.00	35.78
1916	N	TRP A 365	79.861	-20.549	21.955	1.00	17.83	1969	N	GLY A 371	88.380	-24.676	39.577	1.00	31.30
1917	CA	TRP A 365	81.196	-20.835	22.405	1.00	20.62	1970	CA	GLY A 371	88.784	-23.771	40.670	1.00	30.93
1918	C	TRP A 365	81.074	-21.135	23.903	1.00	22.44	1971	C	GLY A 371	87.571	-22.927	41.091	1.00	32.19
1919	O	TRP A 365	80.263	-20.458	24.568	1.00	22.38	1972	O	GLY A 371	86.518	-22.988	40.453	1.00	30.29
1920	CB	TRP A 365	82.167	-19.660	22.183	1.00	19.73	1973	N	ASN A 372	87.725	-22.211	42.194	1.00	31.23
1921	CG	TRP A 365	82.409	-19.420	20.718	1.00	20.76	1974	CA	ASN A 372	86.626	-21.395	42.752	1.00	31.68
1922	CD1	TRP A 365	81.510	-18.888	19.822	1.00	19.99	1975	C	ASN A 372	86.774	-19.969	42.243	1.00	28.25
1923	CD2	TRP A 365	83.597	-19.712	19.980	1.00	20.44	1976	O	ASN A 372	87.724	-19.265	42.643	1.00	28.03
1924	NE1	TRP A 365	82.068	-18.850	18.572	1.00	20.24	1977	CB	ASN A 372	86.716	-21.406	44.286	1.00	33.96
1925	CE2	TRP A 365	83.351	-19.360	18.646	1.00	21.78	1978	CG	ASN A 372	85.534	-20.773	44.992	1.00	36.29
1926	CE3	TRP A 365	84.852	-20.236	20.320	1.00	22.22	1979	OD1	ASN A 372	84.864	-19.865	44.493	1.00	35.90
1927	CZ2	TRP A 365	84.325	-19.484	17.645	1.00	21.66	1980	ND2	ASN A 372	85.211	-21.241	46.212	1.00	35.53
1928	CZ3	TRP A 365	85.821	-20.393	19.335	1.00	22.86	1981	N	LEU A 373	85.865	-19.526	41.377	1.00	25.26
1929	CH2	TRP A 366	85.540	-20.011	18.007	1.00	23.02	1982	CA	LEU A 373	86.006	-18.204	40.775	1.00	23.40
1930	N	LVS A 366	81.789	-22.120	24.428	1.00	22.80	1983	C	LEU A 373	85.148	-17.151	41.456	1.00	22.75
1931	CA	LVS A 366	81.671	-22.479	25.839	1.00	23.01	1984	O	LEU A 373	84.924	-16.071	40.902	1.00	20.78
1932	C	LVS A 366	83.034	-22.735	26.462	1.00	24.27	1985	CB	LEU A 373	85.754	-18.243	39.260	1.00	23.70
1933	O	LVS A 366	84.052	-22.851	25.763	1.00	22.69	1986	CG	LEU A 373	86.733	-19.077	38.413	1.00	24.26
1934	CB	LVS A 366	80.802	-23.755	25.943	1.00	23.05	1987	CD1	LEU A 373	86.538	-18.827	36.918	1.00	24.86
1935	CG	LVS A 366	81.567	-25.016	25.499	1.00	23.62	1988	CD2	LEU A 373	88.185	-18.745	38.729	1.00	26.18
1936	CD	LVS A 366	80.702	-26.253	25.725	1.00	25.72	1989	N	GLU A 374	84.705	-17.422	42.691	1.00	22.76
1937	CE	LVS A 366	81.449	-27.535	25.340	1.00	28.42	1990	CA	GLU A 374	83.955	-16.376	43.386	1.00	20.88
1938	NZ	LVS A 366	80.483	-28.675	25.518	1.00	30.63	1991	C	GLU A 374	84.658	-15.013	43.353	1.00	21.01
1939	N	LEU A 367	83.102	-22.838	27.785	1.00	24.03	1992	O	GLU A 374	85.868	-14.894	43.493	1.00	18.90
1940	CA	LEU A 367	84.359	-23.148	28.478	1.00	23.96	1993	CB	GLU A 374	83.722	-16.806	44.835	1.00	23.51
1941	C	LEU A 367	84.084	-23.398	29.967	1.00	25.05	1994	CG	GLU A 374	82.766	-15.862	45.565	1.00	25.57
1942	O	LEU A 367	83.301	-22.711	30.631	1.00	20.92	1995	CD	GLU A 374	82.144	-16.577	46.741	1.00	29.28
1943	CB	LEU A 367	85.480	-22.129	28.320	1.00	24.83	1996	OE1	GLU A 374	82.604	-17.657	47.084	1.00	29.30
1944	CG	LEU A 367	86.823	-22.510	28.968	1.00	24.39	1997	OE2	GLU A 374	81.193	-16.042	47.307	1.00	27.72
1945	CD1	LEU A 367	87.419	-23.727	28.264	1.00	24.41	1998	N	ASN A 375	83.841	-13.965	43.118	1.00	19.21
1946	CD2	LEU A 367	87.859	-21.399	28.947	1.00	22.93	1999	C	ASN A 375	84.357	-12.596	43.101	1.00	19.30
1947	N	GLN A 368	84.576	-24.553	30.440	1.00	26.14	2000	CA	ASN A 375	85.512	-12.400	42.116	1.00	19.99
1948	CA	GLN A 368	84.447	-24.893	31.849	1.00	27.03	2001	O	ASN A 375	86.381	-11.553	42.288	1.00	18.96
1949	C	GLN A 368	85.791	-24.611	32.529	1.00	26.26	2002	CB	ASN A 375	84.810	-12.224	44.515	1.00	21.23
1950	O	GLN A 368	86.816	-25.102	32.007	1.00	23.19	2003	CG	ASN A 375	83.658	-12.390	45.469	1.00	22.98
1951	CB	GLN A 368	84.045	-26.354	32.059	1.00	29.88	2004	OD1	ASN A 375	83.828	-12.711	46.642	1.00	21.72
1952	CG	GLN A 368	83.942	-26.621	33.557	1.00	34.12	2005	ND2	ASN A 375	82.446	-12.157	44.937	1.00	19.08
1953	CD	GLN A 368	83.326	-27.947	33.888	1.00	38.21	2006	N	TRP A 376	85.534	-13.250	41.077	1.00	18.63
1954	OE1	GLN A 368	82.163	-28.268	33.661	1.00	41.75	2007	CA	TRP A 376	86.479	-13.023	39.991	1.00	20.31
1955	NE2	GLN A 368	84.076	-28.846	34.488	1.00	39.92	2008	C	TRP A 376	85.908	-12.050	38.948	1.00	20.90

2009	O	TRP A 376	84.705	-11.885	38.809	1.00	20.95	2062	CZ	TYR A 380	81.011	-15.013	28.134	1.00	17.98
2010	CB	TRP A 376	86.796	-14.374	39.348	1.00	21.71	2063	OH	TYR A 380	80.229	-15.823	28.913	1.00	16.91
2011	CG	TRP A 376	87.964	-15.000	40.012	1.00	22.49	2064	N	GLN A 381	86.621	-11.910	24.682	1.00	18.61
2012	CD1	TRP A 376	88.036	-15.457	41.347	1.00	20.13	2065	CA	GLN A 381	87.401	-11.198	23.645	1.00	19.39
2013	CD2	TRP A 376	89.290	-15.156	39.450	1.00	22.92	2066	C	GLN A 381	86.998	-11.824	22.307	1.00	17.85
2014	NE1	TRP A 376	89.280	-15.887	41.683	1.00	20.87	2067	O	GLN A 381	87.207	-13.010	22.046	1.00	17.98
2015	CE2	TRP A 376	90.116	-15.690	40.471	1.00	22.98	2068	CB	GLN A 381	88.897	-11.285	23.867	1.00	19.69
2016	CE3	TRP A 376	89.839	-14.871	38.203	1.00	23.59	2069	CG	GLN A 381	89.727	-10.637	22.755	1.00	22.60
2017	CZ2	TRP A 376	91.464	-15.903	40.230	1.00	23.06	2070	CD	GLN A 381	91.215	-10.720	23.077	1.00	26.02
2018	CZ3	TRP A 376	91.187	-15.088	37.962	1.00	24.45	2071	OE1	GLN A 381	91.901	-11.578	22.528	1.00	29.96
2019	CH2	TRP A 376	92.005	-15.606	38.983	1.00	23.52	2072	NE2	GLN A 381	91.773	-9.888	23.933	1.00	24.48
2020	N	TYR A 377	86.618	-11.303	38.111	1.00	19.49	2073	N	VAL A 382	86.238	-11.084	21.522	1.00	16.71
2021	CA	TYR A 377	86.016	-10.505	37.051	1.00	19.50	2074	CA	VAL A 382	85.570	-11.634	20.346	1.00	16.94
2022	C	TYR A 377	86.358	-11.145	35.703	1.00	20.68	2075	C	VAL A 382	86.212	-11.103	19.051	1.00	17.81
2023	O	TYR A 377	87.330	-11.914	35.605	1.00	19.41	2076	O	VAL A 382	86.315	-9.892	18.865	1.00	17.01
2024	CB	TYR A 377	86.409	-9.027	37.144	1.00	17.91	2077	CB	VAL A 382	84.070	-11.250	20.358	1.00	17.30
2025	CG	TYR A 377	85.956	-8.348	38.427	1.00	18.83	2078	CG1	VAL A 382	83.329	-11.902	19.195	1.00	15.09
2026	CD1	TYR A 377	86.708	-8.461	39.604	1.00	19.72	2079	CG2	VAL A 382	83.383	-11.617	21.704	1.00	15.18
2027	CD2	TYR A 377	84.808	-7.586	38.514	1.00	17.93	2080	N	THR A 383	86.582	-12.029	18.170	1.00	17.62
2028	CE1	TYR A 377	86.334	-7.877	40.796	1.00	18.37	2081	CA	THR A 383	87.183	-11.717	16.889	1.00	18.58
2029	CE2	TYR A 377	84.394	-6.978	39.692	1.00	17.34	2082	C	THR A 383	86.147	-11.913	15.773	1.00	20.31
2030	CZ	TYR A 377	85.181	-7.130	40.849	1.00	20.22	2083	O	THR A 383	85.654	-13.000	15.528	1.00	20.06
2031	OH	TYR A 377	84.783	-6.517	42.039	1.00	15.40	2084	CB	THR A 383	88.445	-12.526	16.483	1.00	15.89
2032	N	TYR A 378	85.628	-10.823	34.626	1.00	20.04	2085	OG1	THR A 383	89.447	-12.219	17.481	1.00	16.62
2033	CA	TYR A 378	85.785	-11.425	33.337	1.00	19.08	2086	CG2	THR A 383	89.035	-12.075	15.135	1.00	16.58
2034	C	TYR A 378	85.235	-10.613	32.166	1.00	19.99	2087	N	VAL A 384	84.757	-10.704	14.157	1.00	22.99
2035	O	TYR A 378	84.354	-9.760	32.334	1.00	20.17	2088	CA	VAL A 384	85.721	-10.804	14.157	1.00	29.90
2036	CB	TYR A 378	85.171	-12.819	33.281	1.00	18.87	2089	C	VAL A 384	85.220	-10.119	12.820	1.00	33.88
2037	CG	TYR A 378	83.675	-13.049	33.109	1.00	19.44	2090	O	VAL A 384	83.356	-8.914	12.654	1.00	35.70
2038	CD1	TYR A 378	83.148	-13.529	31.906	1.00	17.38	2091	CB	VAL A 384	83.363	-10.325	14.691	1.00	30.03
2039	CD2	TYR A 378	82.794	-12.845	34.175	1.00	17.88	2092	CG1	VAL A 384	82.464	-10.504	13.470	1.00	29.72
2040	CE1	TYR A 378	81.784	-13.770	31.768	1.00	18.82	2093	CG2	VAL A 384	82.691	-10.944	15.902	1.00	28.84
2041	CE2	TYR A 378	81.431	-13.071	34.036	1.00	18.35	2094	N	ASN A 385	85.449	-11.060	11.887	1.00	20.00
2042	CZ	TYR A 378	80.926	-13.553	32.837	1.00	17.91	2095	CA	ASN A 385	85.893	-10.615	10.580	1.00	20.00
2043	OH	TYR A 378	79.558	-13.797	32.732	1.00	18.43	2096	C	ASN A 385	87.128	-9.723	10.723	1.00	20.00
2044	N	LEU A 379	85.839	-10.897	30.993	1.00	17.82	2097	O	ASN A 385	87.146	-8.572	10.307	1.00	20.00
2045	CA	LEU A 379	85.409	-10.274	29.738	1.00	17.08	2098	CB	ASN A 385	84.918	-10.260	9.442	1.00	20.00
2046	C	LEU A 379	85.510	-11.341	28.635	1.00	18.66	2099	CG	ASN A 385	85.367	-9.925	8.043	1.00	20.00
2047	O	LEU A 379	86.145	-12.370	28.873	1.00	15.93	2100	OD1	ASN A 385	86.415	-10.419	7.638	1.00	20.00
2048	CB	LEU A 379	86.246	-9.088	29.300	1.00	17.38	2101	ND2	ASN A 385	84.535	-9.219	7.259	1.00	20.00
2049	CG	LEU A 379	86.193	-7.747	30.010	1.00	19.69	2102	N	GLY A 386	88.171	-10.355	11.286	1.00	20.00
2050	CD1	LEU A 379	87.317	-6.812	29.589	1.00	16.36	2103	CA	GLY A 386	89.376	-9.584	11.526	1.00	20.00
2051	CD2	LEU A 379	84.837	-7.062	29.750	1.00	18.77	2104	C	GLY A 386	89.506	-8.487	12.584	1.00	20.00
2052	N	TYR A 380	84.730	-11.180	27.547	1.00	19.37	2105	O	GLY A 386	90.579	-7.957	12.839	1.00	20.00
2053	CA	TYR A 380	84.862	-12.039	26.387	1.00	19.03	2106	N	THR A 387	88.331	-8.168	13.157	1.00	38.04
2054	C	TYR A 380	85.691	-11.243	25.346	1.00	19.03	2107	CA	THR A 387	88.344	-7.159	14.198	1.00	34.81
2055	O	TYR A 380	85.468	-10.031	25.169	1.00	20.13	2108	C	THR A 387	87.955	-7.470	15.656	1.00	29.35
2056	CB	TYR A 380	83.558	-12.495	25.715	1.00	17.35	2109	O	THR A 387	86.789	-7.590	16.010	1.00	25.60
2057	CG	TYR A 380	82.665	-13.391	26.562	1.00	17.93	2110	CB	THR A 387	87.528	-5.883	13.919	1.00	35.26
2058	CD1	TYR A 380	81.332	-13.060	26.782	1.00	17.57	2111	OG1	THR A 387	88.115	-5.484	12.678	1.00	38.62
2059	CD2	TYR A 380	83.146	-14.541	27.170	1.00	16.75	2112	CG2	THR A 387	87.395	-4.652	14.820	1.00	35.18
2060	CE2	TYR A 380	80.485	-13.866	27.548	1.00	18.52	2113	N	THR A 388	88.985	-7.660	16.494	1.00	25.85
2061	CE2	TYR A 380	82.344	-15.343	27.948	1.00	17.90	2114	CA	THR A 388	88.710	-8.130	17.839	1.00	22.57

2115	C	THR A 388	88.537	-6.958	18.802	1.00	23.19	2168	CG	TYR A 395	72.739	-14.174	29.709	1.00	14.68
2116	O	THR A 388	89.230	-5.952	18.738	1.00	19.61	2169	CD1	TYR A 395	71.590	-14.846	30.151	1.00	16.46
2117	CB	THR A 388	89.885	-9.000	18.298	1.00	23.33	2170	CD2	TYR A 395	72.836	-13.828	28.360	1.00	14.83
2118	OG1	THR A 388	90.119	-10.030	17.334	1.00	21.46	2171	CE1	TYR A 395	70.576	-15.175	29.276	1.00	13.85
2119	CG2	THR A 388	89.580	-9.641	19.654	1.00	22.30	2172	CE2	TYR A 395	71.820	-14.169	27.441	1.00	14.80
2120	N	GLN A 389	87.527	-7.200	19.658	1.00	20.00	2173	CZ	TYR A 395	70.691	-14.792	27.935	1.00	15.21
2121	CA	GLN A 389	87.071	-6.338	20.720	1.00	22.51	2174	OH	TYR A 395	69.637	-15.146	27.113	1.00	15.56
2122	C	GLN A 389	86.719	-7.159	21.964	1.00	20.76	2175	N	ALA A 396	75.632	-11.307	32.568	1.00	16.64
2123	O	GLN A 389	86.488	-8.371	21.900	1.00	19.22	2176	CA	ALA A 396	76.260	-11.116	33.880	1.00	17.32
2124	CB	GLN A 389	85.816	-5.511	20.338	1.00	24.03	2177	C	ALA A 396	75.211	-10.694	34.933	1.00	18.30
2125	CG	GLN A 389	85.997	-4.637	19.092	1.00	24.14	2178	O	ALA A 396	74.298	-9.914	34.629	1.00	15.51
2126	OD	GLN A 389	84.826	-3.772	18.742	1.00	25.61	2179	CB	ALA A 396	77.260	-9.939	33.770	1.00	17.84
2127	OE1	GLN A 389	84.635	-2.750	19.381	1.00	25.60	2180	N	ARG A 397	75.388	-11.057	36.198	1.00	16.48
2128	NE2	GLN A 389	83.968	-4.122	17.762	1.00	26.31	2181	CA	ARG A 397	74.538	-10.729	37.300	1.00	15.87
2129	N	THR A 390	86.593	-6.495	23.107	1.00	20.02	2182	C	ARG A 397	75.103	-9.694	38.274	1.00	18.12
2130	CA	THR A 390	86.149	-7.117	24.347	1.00	17.35	2183	O	ARG A 397	74.380	-9.284	39.196	1.00	15.59
2131	C	THR A 390	84.749	-6.591	24.716	1.00	18.81	2184	CB	ARG A 397	74.185	-12.040	38.027	1.00	18.60
2132	O	THR A 390	84.358	-5.465	24.384	1.00	17.69	2185	CG	ARG A 397	73.784	-13.316	37.287	1.00	19.84
2133	CB	THR A 390	87.071	-6.834	25.557	1.00	17.85	2186	NE	ARG A 397	72.553	-13.420	36.379	1.00	24.90
2134	OG1	THR A 390	87.007	-5.414	25.809	1.00	18.20	2187	CZ	ARG A 397	71.025	-14.402	35.008	1.00	22.76
2135	CG2	THR A 390	88.505	-7.265	25.256	1.00	17.70	2188	NH1	ARG A 397	70.886	-13.392	34.144	1.00	19.94
2136	N	ALA A 391	84.004	-7.388	25.445	1.00	17.61	2189	NH2	ARG A 397	70.123	-15.367	35.053	1.00	23.58
2137	CA	ALA A 391	82.657	-7.095	25.890	1.00	18.43	2190	NH2	ARG A 397	70.123	-15.367	35.053	1.00	16.37
2138	C	ALA A 391	82.254	-7.783	27.192	1.00	17.62	2191	N	ALA A 398	76.346	-9.296	38.010	1.00	16.37
2139	O	ALA A 391	82.712	-8.896	27.470	1.00	17.18	2192	CA	ALA A 398	77.067	-8.350	38.855	1.00	17.06
2140	CB	ALA A 391	81.673	-7.613	24.811	1.00	16.39	2193	C	ALA A 398	78.247	-7.820	38.038	1.00	15.40
2141	N	VAL A 392	81.382	-7.128	27.942	1.00	17.34	2194	O	ALA A 398	78.597	-8.413	37.006	1.00	15.82
2142	CA	VAL A 392	80.822	-7.676	29.180	1.00	15.98	2195	CB	ALA A 398	77.565	-9.054	40.119	1.00	16.67
2143	C	VAL A 392	79.722	-8.661	28.776	1.00	15.84	2196	N	ILE A 399	78.785	-6.669	38.345	1.00	15.06
2144	O	VAL A 392	79.002	-8.376	27.793	1.00	16.85	2197	CA	ILE A 399	79.836	-6.039	37.572	1.00	15.89
2145	CB	VAL A 392	80.205	-6.584	30.070	1.00	15.95	2198	C	ILE A 399	80.901	-5.366	38.448	1.00	17.93
2146	CG1	VAL A 392	79.490	-7.180	31.301	1.00	15.89	2199	O	ILE A 399	80.735	-5.221	39.663	1.00	15.09
2147	CG2	VAL A 392	81.266	-5.543	30.482	1.00	15.39	2200	CB	ILE A 399	79.242	-4.896	36.717	1.00	15.87
2148	N	ASP A 393	79.650	-9.799	29.422	1.00	15.45	2201	CG1	ILE A 399	78.242	-4.078	37.530	1.00	16.12
2149	CA	ASP A 393	78.587	-10.790	29.162	1.00	16.16	2202	CG2	ILE A 399	77.845	-2.740	36.874	1.00	16.62
2150	C	ASP A 393	77.217	-10.175	29.367	1.00	15.39	2203	CD1	ILE A 399	81.929	-4.847	37.736	1.00	16.57
2151	O	ASP A 393	76.864	-9.706	30.471	1.00	14.42	2204	N	SER A 400	82.921	-3.993	38.409	1.00	15.56
2152	CB	ASP A 393	78.802	-11.946	30.158	1.00	14.87	2205	CA	SER A 400	82.236	-2.619	38.438	1.00	17.27
2153	CG	ASP A 393	78.031	-13.211	29.948	1.00	16.08	2206	C	SER A 400	82.236	-2.619	38.438	1.00	16.46
2154	OD1	ASP A 393	78.506	-14.295	30.403	1.00	16.54	2207	O	SER A 400	81.271	-2.466	37.653	1.00	15.65
2155	OD2	ASP A 393	76.950	-13.261	29.285	1.00	17.16	2208	CB	SER A 400	84.181	-3.946	37.561	1.00	15.65
2156	N	PRO A 394	76.340	-10.247	28.378	1.00	16.89	2209	OG	SER A 400	83.953	-3.310	36.304	1.00	15.40
2157	CA	PRO A 394	74.976	-9.706	28.510	1.00	18.08	2210	N	VAL A 401	82.765	-1.616	39.082	1.00	15.63
2158	C	PRO A 394	74.160	-10.345	29.626	1.00	17.40	2211	CA	VAL A 401	82.217	-0.260	39.027	1.00	16.67
2159	O	PRO A 394	73.183	-9.757	30.116	1.00	17.22	2212	C	VAL A 401	82.096	0.223	37.617	1.00	18.39
2160	CB	PRO A 394	74.341	-9.948	27.148	1.00	16.39	2213	O	VAL A 401	83.057	0.177	36.827	1.00	19.89
2161	CG	PRO A 394	75.545	-9.916	26.223	1.00	18.52	2214	CB	VAL A 401	83.072	0.692	39.881	1.00	17.74
2162	CD	PRO A 394	76.619	-10.675	26.975	1.00	17.04	2215	CG1	VAL A 401	82.552	2.095	39.678	1.00	16.22
2163	N	TYR A 395	74.517	-11.568	30.006	1.00	16.37	2216	CG2	VAL A 401	83.009	0.220	41.367	1.00	16.84
2164	CA	TYR A 395	73.877	-12.321	31.086	1.00	16.64	2217	N	ASN A 402	80.936	0.785	37.203	1.00	19.45
2165	C	TYR A 395	74.578	-12.142	32.436	1.00	16.49	2218	CA	ASN A 402	80.780	1.251	35.824	1.00	19.83
2166	O	TYR A 395	74.184	-12.763	33.421	1.00	15.61	2219	C	ASN A 402	80.895	0.145	34.794	1.00	19.97
2167	CB	TYR A 395	73.809	-13.820	30.721	1.00	16.31	2220	O	ASN A 402	81.048	0.448	33.599	1.00	19.00

77.237	-12.727	41.871	1.00	18.02
78.372	-15.587	44.041	1.00	21.46
77.548	-16.630	44.651	1.00	23.20
76.213	-15.995	45.035	1.00	22.82
76.182	-15.290	46.065	1.00	22.94
78.239	-17.131	45.946	1.00	23.65
77.474	-18.262	46.611	1.00	24.86
76.311	-18.535	46.249	1.00	25.50
78.060	-18.934	47.490	1.00	27.15
75.146	-16.167	44.271	1.00	21.42
73.882	-15.508	44.506	1.00	21.38
73.237	-15.851	45.845	1.00	22.44
72.566	-14.989	46.436	1.00	19.95
72.876	-15.820	43.360	1.00	20.60
73.222	-15.156	42.010	1.00	20.02
72.363	-15.723	40.952	1.00	16.46
73.133	-13.644	42.152	1.00	19.54
73.413	-17.079	46.331	1.00	21.58
72.795	-16.452	47.612	1.00	22.40
73.254	-16.679	48.824	1.00	22.02
72.506	-16.191	49.703	1.00	22.52
73.028	-18.966	47.842	1.00	26.92
72.311	-19.472	49.084	1.00	31.49
70.825	-19.669	48.788	1.00	33.84
70.110	-19.953	50.118	1.00	37.42
70.382	-18.751	50.970	1.00	40.45
74.517	-16.248	48.810	1.00	18.93
75.194	-15.455	49.803	1.00	20.77
74.716	-14.003	49.860	1.00	20.66
74.909	-13.273	50.842	1.00	21.58
76.696	-15.412	49.507	1.00	19.90
74.083	-13.550	48.779	1.00	19.42
73.566	-12.207	48.706	1.00	20.42
72.181	-12.039	49.330	1.00	22.20
71.750	-10.883	49.514	1.00	20.49
73.489	-11.665	47.263	1.00	20.49
72.430	-12.401	46.619	1.00	21.35
74.770	-11.821	46.451	1.00	19.00
71.470	-13.097	49.627	1.00	21.64
70.149	-13.115	50.208	1.00	21.34
70.129	-12.642	51.661	1.00	20.48
70.955	-13.100	52.457	1.00	21.23
69.544	-14.522	50.278	1.00	21.16
69.327	-15.177	48.937	1.00	23.55
69.131	-14.154	47.881	1.00	22.37
69.342	-16.414	48.905	1.00	24.37
69.298	-11.654	51.921	1.00	18.99
69.131	-11.131	53.268	1.00	18.59
68.487	-12.203	54.143	1.00	19.83
67.848	-13.131	53.613	1.00	16.95
68.177	-9.955	53.092	1.00	18.50
67.383	-10.255	51.848	1.00	18.19
68.355	-11.017	50.963	1.00	18.15

2327	N	ALA A 417	58.584	-12.001	55.459	1.00	19.41	2380	NE2	HIS A 423	51.519	-15.838	49.939	1.00	58.38
2328	CA	ALA A 417	67.928	-12.898	56.410	1.00	18.88	2381	N	GLU A 424	55.414	-13.228	47.961	1.00	43.93
2329	C	ALA A 417	66.416	-12.866	56.226	1.00	19.84	2382	CA	GLU A 424	54.955	-12.662	46.717	1.00	41.46
2330	O	ALA A 417	65.795	-11.828	55.964	1.00	19.83	2383	C	GLU A 424	53.561	-12.097	47.029	1.00	35.89
2331	CB	ALA A 417	68.258	-12.437	57.822	1.00	18.37	2384	O	GLU A 424	52.765	-12.666	47.764	1.00	32.50
2332	N	GLY A 418	65.790	-14.020	56.379	1.00	21.41	2385	CB	GLU A 424	54.860	-13.614	45.537	1.00	45.39
2333	CA	GLY A 418	64.368	-14.233	56.237	1.00	23.22	2386	CG	GLU A 424	53.602	-14.436	45.385	1.00	50.15
2334	C	GLY A 418	63.846	-14.337	54.810	1.00	23.60	2387	CD	GLU A 424	53.588	-15.845	45.929	1.00	53.14
2335	O	GLY A 418	62.643	-14.572	54.590	1.00	22.08	2388	OE1	GLU A 424	52.472	-16.435	45.889	1.00	55.07
2336	N	TRP A 419	64.710	-14.183	53.807	1.00	23.46	2389	OE2	GLU A 424	54.628	-16.378	46.392	1.00	54.61
2337	CA	TRP A 419	64.402	-14.234	52.396	1.00	23.20	2390	N	GLN A 425	53.341	-10.927	46.478	1.00	31.51
2338	C	TRP A 419	63.606	-15.472	52.012	1.00	25.42	2391	CA	GLN A 425	52.114	-10.187	46.730	1.00	30.43
2339	O	TRP A 419	62.668	-15.373	51.199	1.00	24.03	2392	C	GLN A 425	51.336	-9.895	45.465	1.00	27.84
2340	CB	TRP A 419	65.670	-14.233	51.530	1.00	22.84	2393	O	GLN A 425	51.444	-8.806	44.889	1.00	25.73
2341	CD1	TRP A 419	65.454	-13.984	50.043	1.00	22.68	2394	CB	GLN A 425	52.513	-8.862	47.412	1.00	28.91
2342	CD2	TRP A 419	65.788	-14.816	48.989	1.00	21.27	2395	CG	GLN A 425	52.923	-9.100	48.863	1.00	31.80
2343	NE1	TRP A 419	64.806	-12.860	49.459	1.00	20.14	2396	CD	GLN A 425	51.701	-9.408	49.711	1.00	34.90
2344	NE2	TRP A 419	65.454	-14.166	47.813	1.00	22.72	2397	OE1	GLN A 425	51.857	-10.238	50.604	1.00	35.50
2345	CB	TRP A 419	64.841	-12.969	48.060	1.00	21.05	2398	NE2	GLN A 425	50.583	-8.779	49.384	1.00	34.92
2346	CE3	TRP A 419	64.233	-11.704	50.009	1.00	21.41	2399	N	THR A 426	50.650	-10.924	44.981	1.00	25.79
2347	CZ2	TRP A 419	64.305	-12.027	47.163	1.00	20.75	2400	CA	THR A 426	49.878	-10.700	43.722	1.00	25.43
2348	CZ3	TRP A 419	63.711	-10.769	49.147	1.00	22.68	2401	C	THR A 426	48.438	-11.054	44.030	1.00	24.91
2349	CH2	TRP A 419	63.761	-10.889	47.753	1.00	21.75	2402	O	THR A 426	48.194	-12.077	44.673	1.00	25.67
2350	N	GLN A 420	63.929	-16.638	52.581	1.00	26.47	2403	CB	THR A 426	50.462	-11.587	42.625	1.00	24.59
2351	CA	GLN A 420	63.179	-17.861	52.325	1.00	29.80	2404	OG1	THR A 426	50.660	-12.926	43.104	1.00	26.94
2352	C	GLN A 420	61.719	-17.770	52.728	1.00	28.92	2405	CG2	THR A 426	51.843	-11.146	42.152	1.00	25.00
2353	O	GLN A 420	60.919	-18.452	52.090	1.00	28.66	2406	N	PRO A 427	47.481	-10.229	43.662	1.00	24.58
2354	CB	GLN A 420	63.849	-19.089	52.961	1.00	33.14	2407	CA	PRO A 427	46.078	-10.493	43.995	1.00	22.44
2355	CG	GLN A 420	64.919	-19.737	52.090	1.00	39.56	2408	C	PRO A 427	45.481	-11.448	42.987	1.00	19.97
2356	CD	GLN A 420	64.607	-19.919	50.614	1.00	41.28	2409	O	PRO A 427	46.143	-11.846	42.015	1.00	18.98
2357	OE1	GLN A 420	65.071	-19.074	49.835	1.00	43.54	2410	CB	PRO A 427	45.449	-9.098	43.970	1.00	22.44
2358	NE2	GLN A 420	63.849	-20.928	50.243	1.00	43.71	2411	CG	PRO A 427	46.215	-8.410	42.886	1.00	23.34
2359	N	GLY A 421	61.326	-16.936	53.690	1.00	29.02	2412	CD	PRO A 427	47.643	-8.943	42.956	1.00	24.22
2360	CA	GLY A 421	59.929	-16.790	54.080	1.00	27.43	2413	N	ALA A 428	44.221	-11.818	43.186	1.00	18.32
2361	C	GLY A 421	59.223	-15.673	53.308	1.00	28.32	2414	CA	ALA A 428	43.524	-12.705	42.287	1.00	18.67
2362	O	GLY A 421	58.048	-15.418	53.556	1.00	24.66	2415	C	ALA A 428	43.302	-12.115	40.901	1.00	18.67
2363	N	ASP A 422	59.878	-15.004	52.358	1.00	28.80	2416	O	ALA A 428	43.391	-12.950	39.990	1.00	18.53
2364	CA	ASP A 422	59.295	-13.889	51.627	1.00	30.89	2417	CB	ALA A 428	42.176	-13.179	42.853	1.00	19.42
2365	C	ASP A 422	58.088	-14.200	50.738	1.00	36.19	2418	N	ASN A 429	43.248	-10.788	40.730	1.00	16.60
2366	O	ASP A 422	58.230	-14.870	49.727	1.00	38.46	2419	CA	ASN A 429	43.080	-10.263	39.358	1.00	15.96
2367	CB	ASP A 422	60.420	-13.227	50.804	1.00	27.10	2420	C	ASN A 429	43.673	-8.877	39.366	1.00	16.94
2368	CG	ASP A 422	59.951	-11.980	50.032	1.00	25.30	2421	O	ASN A 429	43.676	-8.221	40.413	1.00	17.66
2369	OD1	ASP A 422	59.222	-11.152	50.594	1.00	23.55	2422	CB	ASN A 429	41.572	-10.199	39.015	1.00	15.37
2370	OD2	ASP A 422	60.287	-11.929	48.830	1.00	22.98	2423	CG	ASN A 429	41.218	-9.874	37.587	1.00	14.52
2371	N	HIS A 423	56.911	-13.629	51.020	1.00	40.93	2424	OD1	ASN A 429	40.864	-10.725	36.749	1.00	17.02
2372	CA	HIS A 423	55.703	-13.849	50.233	1.00	47.21	2425	ND2	ASN A 429	41.224	-8.619	37.164	1.00	12.11
2373	C	HIS A 423	55.313	-12.763	49.209	1.00	45.35	2426	N	PRO A 430	44.223	-8.379	38.259	1.00	17.36
2374	O	HIS A 423	54.768	-11.681	49.406	1.00	47.07	2427	CA	PRO A 430	44.798	-7.059	38.201	1.00	17.36
2375	CB	HIS A 423	54.512	-14.100	51.176	1.00	51.41	2428	C	PRO A 430	43.884	-5.954	38.671	1.00	16.98
2376	CG	HIS A 423	53.238	-14.617	50.601	1.00	56.12	2429	O	PRO A 430	44.439	-4.967	39.171	1.00	15.58
2377	ND1	HIS A 423	52.275	-13.795	50.033	1.00	58.05	2430	CB	PRO A 430	45.274	-6.889	36.756	1.00	17.72
2378	CD2	HIS A 423	52.745	-15.896	50.562	1.00	57.47	2431	CG	PRO A 430	45.459	-8.315	36.305	1.00	17.97
2379	CE1	HIS A 423	51.265	-14.568	49.639	1.00	58.60	2432	CD	PRO A 430	44.377	-9.110	36.977	1.00	16.18

2433	N	VAL	A	431	42.554	-5.999	38.575	1.00	16.77	55.651	5.927	41.411	1.00	16.03
2434	CA	VAL	A	431	41.696	-4.882	39.029	1.00	14.93	55.329	7.076	41.747	1.00	17.07
2435	C	VAL	A	431	41.724	-4.718	40.549	1.00	16.96	54.458	5.834	39.263	1.00	15.08
2436	O	VAL	A	431	41.207	-3.711	41.066	1.00	14.124	55.716	5.978	38.411	1.00	14.65
2437	CB	VAL	A	431	40.236	-5.000	38.552	1.00	14.61	55.493	6.596	37.048	1.00	14.65
2438	CG1	VAL	A	431	40.141	-5.164	37.018	1.00	11.37	54.648	7.489	36.869	1.00	15.22
2439	CG2	VAL	A	431	39.470	-6.174	39.204	1.00	9.63	56.087	6.145	36.035	1.00	16.08
2440	N	ASP	A	432	42.285	-5.672	41.303	1.00	15.55	56.882	5.394	41.543	1.00	13.82
2441	CA	ASP	A	432	42.506	-5.742	42.728	1.00	16.36	57.878	6.186	42.253	1.00	13.55
2442	C	ASP	A	432	43.735	-4.744	43.102	1.00	16.54	59.312	5.910	41.823	1.00	14.91
2443	O	ASP	A	432	43.956	-4.499	44.305	1.00	15.51	59.721	4.775	41.558	1.00	13.87
2444	CB	ASP	A	432	42.669	-6.988	43.365	1.00	14.88	57.660	5.898	43.765	1.00	13.69
2445	CG	ASP	A	432	41.447	-7.835	43.087	1.00	15.34	61.572	6.963	41.828	1.00	16.29
2446	OD1	ASP	A	432	40.318	-7.267	43.043	1.00	16.21	62.351	6.603	42.805	1.00	16.70
2447	OD2	ASP	A	432	41.488	-9.064	42.873	1.00	14.61	62.025	7.212	43.813	1.00	14.31
2448	N	GLU	A	433	44.537	-4.259	42.145	1.00	15.94	62.043	8.086	40.776	1.00	16.30
2449	CA	GLU	A	433	45.689	-3.429	42.512	1.00	16.94	63.440	8.147	40.223	1.00	16.75
2450	C	GLU	A	433	45.343	-1.946	42.441	1.00	16.06	64.518	8.470	41.049	1.00	14.58
2451	O	GLU	A	433	44.479	-1.513	41.664	1.00	16.07	63.943	7.963	38.965	1.00	15.99
2452	CB	GLU	A	433	46.942	-3.630	41.625	1.00	15.85	65.624	8.516	40.288	1.00	17.06
2453	CG	GLU	A	433	47.546	-5.015	41.739	1.00	16.52	65.302	8.221	39.029	1.00	16.41
2454	CD	GLU	A	433	48.933	-5.312	41.195	1.00	16.36	63.328	5.687	42.858	1.00	15.20
2455	OE1	GLU	A	433	49.492	-4.536	40.379	1.00	11.53	64.031	5.389	44.106	1.00	15.25
2456	OE2	GLU	A	433	49.449	-6.397	41.635	1.00	14.91	64.653	6.618	44.780	1.00	16.03
2457	N	VAL	A	434	46.021	-1.168	43.262	1.00	15.28	64.516	6.773	45.999	1.00	16.04
2458	CA	VAL	A	434	46.036	0.299	43.193	1.00	14.14	65.116	4.317	43.867	1.00	15.02
2459	C	VAL	A	434	47.553	0.628	43.106	1.00	15.28	65.972	4.169	45.128	1.00	16.66
2460	O	VAL	A	434	48.292	0.509	44.136	1.00	13.41	64.459	2.977	43.508	1.00	15.14
2461	CB	VAL	A	434	45.360	0.930	44.419	1.00	14.74	65.342	7.469	44.034	1.00	16.63
2462	CG1	VAL	A	434	43.954	0.334	44.672	1.00	13.12	65.925	8.698	44.541	1.00	17.10
2463	CG2	VAL	A	434	43.954	0.334	44.672	1.00	13.12	65.925	8.698	44.541	1.00	17.10
2464	N	ILE	A	435	48.014	1.058	41.947	1.00	14.64	64.899	9.740	45.000	1.00	17.74
2465	CA	ILE	A	435	49.459	1.202	41.665	1.00	13.40	65.010	10.221	46.170	1.00	17.74
2466	C	ILE	A	435	49.459	1.202	41.665	1.00	13.40	65.010	10.221	46.170	1.00	17.74
2467	O	ILE	A	435	49.312	3.525	41.875	1.00	15.38	66.896	9.304	43.501	1.00	14.61
2468	CB	ILE	A	435	49.775	0.758	40.228	1.00	14.42	67.704	10.461	44.088	1.00	16.94
2469	CG1	ILE	A	435	51.253	-0.693	40.023	1.00	14.98	68.732	11.060	43.137	1.00	18.60
2470	CG2	ILE	A	435	51.253	-0.693	40.023	1.00	14.98	68.732	11.060	43.137	1.00	18.60
2471	CD1	ILE	A	435	49.227	-1.169	38.568	1.00	13.44	71.094	11.121	44.855	1.00	17.67
2472	N	TYR	A	436	51.082	2.759	42.563	1.00	13.59	71.094	11.121	44.855	1.00	17.67
2473	CA	TYR	A	436	51.698	4.037	42.855	1.00	15.25	71.002	13.363	44.893	1.00	17.22
2474	C	TYR	A	436	53.109	4.093	42.264	1.00	15.01	63.897	10.087	44.191	1.00	16.68
2475	O	TYR	A	436	53.988	3.279	42.617	1.00	14.02	62.882	11.067	44.550	1.00	17.07
2476	CB	TYR	A	436	51.711	4.156	44.367	1.00	15.52	62.150	10.781	45.865	1.00	15.50
2477	CG	TYR	A	436	52.196	5.355	45.116	1.00	16.16	61.789	11.686	46.627	1.00	14.92
2478	CD1	TYR	A	436	51.289	6.303	45.576	1.00	15.41	61.705	11.140	43.534	1.00	16.09
2479	CD2	TYR	A	436	53.498	5.498	45.460	1.00	15.75	62.092	11.481	42.103	1.00	18.27
2480	CE1	TYR	A	436	51.717	7.384	46.327	1.00	16.02	61.161	11.472	41.265	1.00	16.61
2481	CE2	TYR	A	436	53.987	6.584	46.218	1.00	15.63	63.293	11.722	41.820	1.00	16.36
2482	CZ	TYR	A	436	53.058	7.496	46.674	1.00	15.39	61.865	9.519	46.113	1.00	14.50
2483	OH	TYR	A	436	53.434	8.562	47.464	1.00	16.13	61.090	9.094	47.277	1.00	14.57
2484	N	GLU	A	437	53.329	4.992	41.304	1.00	15.46	61.629	9.580	48.615	1.00	16.96
2485	CA	GLU	A	437	54.622	5.123	40.620	1.00	15.46	60.820	9.958	48.474	1.00	15.43
2486										61.104	7.553	47.333	1.00	15.23
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2539	CG	PHE A 443	60.077	7.005	48.292	1.00	16.07	2592	C	MET A 451	66.056	8.859	56.152	1.00	21.41
2540	CD1	PHE A 443	60.475	6.290	49.410	1.00	17.87	2593	O	MET A 451	66.534	9.886	55.659	1.00	21.59
2541	CD2	PHE A 443	58.722	7.225	48.081	1.00	17.50	2594	CB	MET A 451	64.044	8.109	54.818	1.00	18.54
2542	CE1	PHE A 443	59.546	5.788	50.302	1.00	19.15	2595	CG	MET A 451	62.704	7.387	54.938	1.00	18.74
2543	CE2	PHE A 443	57.797	6.682	48.961	1.00	19.87	2596	SD	MET A 451	61.951	7.071	53.330	1.00	15.90
2544	CZ	PHE A 443	58.202	5.978	50.077	1.00	19.27	2597	CE	MET A 451	61.313	8.726	52.990	1.00	16.43
2545	N	SER A 444	62.941	9.578	48.844	1.00	14.65	2598	N	LYS A 452	66.849	7.964	56.728	1.00	24.96
2546	CA	SER A 444	10.014	50.121	50.121	1.00	16.85	2599	CA	LYS A 452	68.292	8.105	56.755	1.00	25.67
2547	C	SER A 444	64.692	10.959	50.081	1.00	17.60	2600	C	LYS A 452	69.007	7.729	55.462	1.00	24.98
2548	O	SER A 444	65.223	11.288	51.168	1.00	17.78	2601	O	LYS A 452	69.976	8.421	55.111	1.00	22.58
2549	CB	SER A 444	63.933	8.772	50.891	1.00	17.91	2602	CB	LYS A 452	68.865	7.134	57.821	1.00	29.87
2550	OG	SER A 444	64.813	8.072	50.004	1.00	18.93	2603	CG	LYS A 452	68.343	7.423	59.227	1.00	34.10
2551	N	ILE A 445	65.083	11.532	48.944	1.00	16.65	2604	CD	LYS A 452	69.048	6.450	60.162	1.00	38.10
2552	CA	ILE A 445	66.272	12.363	48.864	1.00	17.86	2605	CE	LYS A 452	68.830	6.729	61.640	1.00	40.92
2553	C	ILE A 445	66.133	13.664	49.641	1.00	19.05	2606	NZ	LYS A 452	69.743	5.855	62.443	1.00	43.49
2554	O	ILE A 445	67.136	14.236	50.089	1.00	19.84	2607	N	ASN A 453	68.621	6.628	54.808	1.00	22.30
2555	CB	ILE A 445	66.725	12.704	47.422	1.00	18.82	2608	CA	ASN A 453	69.323	6.230	53.583	1.00	22.25
2556	CG1	ILE A 445	68.114	13.345	47.373	1.00	19.76	2609	C	ASN A 453	68.792	6.986	52.372	1.00	22.88
2557	CG2	ILE A 445	65.717	13.625	46.737	1.00	16.03	2610	O	ASN A 453	68.213	6.412	51.448	1.00	20.10
2558	CD1	ILE A 445	69.261	12.451	47.830	1.00	17.68	2611	CB	ASN A 453	69.185	4.732	53.390	1.00	22.17
2559	N	ASP A 446	64.944	14.247	49.757	1.00	19.31	2612	CG	ASN A 453	69.885	3.894	54.438	1.00	22.47
2560	CA	ASP A 446	64.795	15.549	50.429	1.00	19.31	2613	OD1	ASN A 453	69.207	3.368	55.345	1.00	26.98
2561	C	ASP A 446	65.343	15.527	51.856	1.00	18.39	2614	ND2	ASN A 453	71.168	3.715	54.360	1.00	18.00
2562	O	ASP A 446	65.028	14.618	52.664	1.00	14.79	2615	N	LYS A 454	69.120	8.272	52.262	1.00	22.54
2563	CB	ASP A 446	63.319	15.965	50.406	1.00	17.77	2616	CA	LYS A 454	68.515	9.200	51.323	1.00	21.14
2564	CG	ASP A 446	62.997	17.404	50.598	1.00	19.68	2617	C	LYS A 454	68.895	8.936	49.881	1.00	20.78
2565	OD1	ASP A 446	62.211	18.007	49.823	1.00	20.47	2618	O	LYS A 454	70.071	8.790	49.545	1.00	22.89
2566	OD2	ASP A 446	63.527	18.071	51.516	1.00	17.16	2619	CB	LYS A 454	68.872	10.638	51.774	1.00	21.38
2567	N	ALA A 447	65.955	16.640	52.293	1.00	19.59	2620	CG	LYS A 454	68.057	11.105	53.013	1.00	23.20
2568	CA	ALA A 447	66.372	16.734	53.696	1.00	20.17	2621	CD	LYS A 454	68.334	12.597	53.277	1.00	23.57
2569	C	ALA A 447	65.212	16.578	54.680	1.00	21.62	2622	CE	LYS A 454	67.796	12.998	54.648	1.00	25.95
2570	O	ALA A 447	65.444	16.179	55.845	1.00	20.80	2623	NZ	LYS A 454	66.341	12.839	54.758	1.00	26.08
2571	CB	ALA A 447	67.086	18.077	53.958	1.00	22.60	2624	N	GLY A 455	67.909	8.715	49.012	1.00	19.05
2572	N	ASN A 448	63.958	16.873	54.328	1.00	20.17	2625	CA	GLY A 455	68.086	8.463	47.590	1.00	17.30
2573	CA	ASN A 448	62.852	16.752	55.303	1.00	19.49	2626	C	GLY A 455	68.350	7.013	47.242	1.00	17.20
2574	C	ASN A 448	62.130	15.408	55.274	1.00	20.38	2627	O	GLY A 455	68.723	6.665	46.111	1.00	17.53
2575	O	ASN A 448	61.062	15.275	55.906	1.00	18.16	2628	N	LYS A 456	68.270	6.123	48.226	1.00	15.28
2576	CB	ASN A 448	61.835	17.863	54.959	1.00	18.25	2629	CA	LYS A 456	68.659	4.734	48.032	1.00	16.32
2577	CG	ASN A 448	61.103	17.701	53.619	1.00	19.72	2630	C	LYS A 456	67.611	3.650	48.265	1.00	15.37
2578	OD1	ASN A 448	61.019	16.634	52.997	1.00	19.01	2631	O	LYS A 456	66.603	3.951	48.904	1.00	15.63
2579	ND2	ASN A 448	60.625	18.786	53.028	1.00	18.34	2632	CB	LYS A 456	69.787	4.424	49.040	1.00	18.28
2580	N	SER A 449	62.630	14.404	54.537	1.00	19.41	2633	CG	LYS A 456	70.918	5.434	49.114	1.00	18.06
2581	CA	SER A 449	61.917	13.131	54.370	1.00	20.28	2634	CD	LYS A 456	72.081	4.992	48.231	1.00	19.93
2582	C	SER A 449	61.780	12.255	55.599	1.00	20.00	2635	CE	LYS A 456	73.093	6.121	48.121	1.00	20.50
2583	O	SER A 449	60.950	11.332	55.677	1.00	20.48	2636	NZ	LYS A 456	74.035	5.934	46.985	1.00	18.68
2584	CB	SER A 449	62.563	12.336	53.203	1.00	18.80	2637	N	TYR A 457	67.870	2.454	47.758	1.00	14.15
2585	OG	SER A 449	63.731	11.616	53.593	1.00	16.39	2638	CA	TYR A 457	66.986	1.341	47.981	1.00	13.53
2586	N	GLY A 450	62.709	12.410	56.516	1.00	19.28	2639	C	TYR A 457	66.678	1.189	49.489	1.00	18.21
2587	CA	GLY A 450	62.812	11.662	57.762	1.00	18.69	2640	O	TYR A 457	65.487	1.011	49.788	1.00	13.29
2588	C	GLY A 450	63.495	10.312	57.606	1.00	19.34	2641	CB	TYR A 457	67.490	-0.024	47.538	1.00	13.55
2589	O	GLY A 450	63.580	9.532	58.586	1.00	19.10	2642	CG	TYR A 457	67.956	-0.142	46.075	1.00	14.83
2590	N	MET A 451	63.897	9.939	56.412	1.00	17.66	2643	CD1	TYR A 457	69.241	-0.546	45.761	1.00	15.53
2591	CA	MET A 451	64.550	8.650	56.169	1.00	19.49	2644	CD2	TYR A 457	67.107	0.110	45.014	1.00	15.14



2645	CE1 TYR A 457	69.663	-0.645	44.409	1.00	15.97	2698	NE2 HIS A 463	58.029	-1.696	58.538	1.00	30.87
2646	CE2 TYR A 457	67.460	0.018	43.665	1.00	15.67	2699	N GLY A 464	58.637	3.962	61.066	1.00	23.85
2647	CZ TYR A 457	68.762	-0.369	43.408	1.00	16.86	2700	CA GLY A 464	58.547	5.049	62.031	1.00	22.89
2648	OH TYR A 457	69.165	-0.482	42.066	1.00	18.18	2701	C GLY A 464	59.042	6.398	61.558	1.00	23.91
2649	N LEU A 458	67.603	1.255	50.450	1.00	17.70	2702	O GLY A 464	59.256	7.293	62.406	1.00	21.28
2650	CA LEU A 458	67.335	0.919	51.869	1.00	18.01	2703	N THR A 465	59.227	6.617	60.250	1.00	21.74
2651	C LEU A 458	66.370	1.882	52.549	1.00	15.81	2704	CA THR A 465	59.815	7.888	59.806	1.00	21.41
2652	O LEU A 458	65.802	1.650	53.669	1.00	14.97	2705	C THR A 465	58.782	8.990	59.735	1.00	21.03
2653	CB LEU A 458	68.678	0.861	52.699	1.00	17.40	2706	O THR A 465	57.602	8.744	59.460	1.00	23.25
2654	CG LEU A 458	69.584	-0.333	52.378	1.00	17.94	2707	CB THR A 465	60.563	7.738	58.467	1.00	22.09
2655	CD1 LEU A 458	70.830	-0.312	53.282	1.00	20.17	2708	OG1 THR A 465	59.630	7.327	57.447	1.00	20.70
2656	CD2 LEU A 458	68.866	-1.692	52.511	1.00	17.60	2709	CG2 THR A 465	61.643	6.667	58.659	1.00	21.72
2657	N ALA A 459	66.132	3.071	51.984	1.00	15.65	2710	N LYS A 466	59.185	10.189	60.070	1.00	19.33
2658	CA ALA A 459	65.167	4.005	52.608	1.00	16.80	2711	CA LYS A 466	58.343	11.334	60.285	1.00	21.71
2659	C ALA A 459	63.772	3.381	52.772	1.00	18.08	2712	C LYS A 466	58.905	12.549	59.557	1.00	21.36
2660	O ALA A 459	63.016	3.656	53.718	1.00	15.52	2713	O LYS A 466	60.121	12.630	59.456	1.00	22.34
2661	CB ALA A 459	65.103	5.260	51.750	1.00	14.58	2714	CB LYS A 466	58.316	11.761	61.775	1.00	22.16
2662	N PHE A 460	63.361	2.510	51.838	1.00	16.60	2715	CG LYS A 466	57.913	10.655	62.722	1.00	25.69
2663	CA PHE A 460	62.117	1.786	51.868	1.00	18.35	2716	CD LYS A 466	56.511	10.112	62.448	1.00	27.19
2664	C PHE A 460	62.017	0.683	52.942	1.00	19.16	2717	CE LYS A 466	56.168	9.053	63.502	1.00	29.76
2665	O PHE A 460	60.944	0.074	53.052	1.00	16.71	2718	NZ LYS A 466	54.932	8.298	63.127	1.00	29.77
2666	CB PHE A 460	61.813	1.132	50.518	1.00	19.39	2719	N GLY A 467	58.029	13.410	59.087	1.00	20.73
2667	CG PHE A 460	60.199	2.064	49.369	1.00	19.42	2720	CA GLY A 467	58.437	14.611	58.385	1.00	22.16
2668	CD1 PHE A 460	62.477	2.748	48.693	1.00	19.19	2721	C GLY A 467	57.855	15.833	59.110	1.00	23.57
2669	CD2 PHE A 460	59.853	2.859	47.787	1.00	20.33	2722	O GLY A 467	57.559	15.770	60.300	1.00	21.29
2670	CE1 PHE A 460	62.162	3.544	47.607	1.00	20.31	2723	N PRO A 468	57.742	16.944	58.387	1.00	24.04
2671	CE2 PHE A 460	60.847	3.590	47.141	1.00	20.55	2724	CA PRO A 468	57.264	18.188	58.952	1.00	24.86
2672	CZ PHE A 460	63.086	0.410	53.727	1.00	17.62	2725	C PRO A 468	55.921	18.023	59.638	1.00	26.71
2673	N THR A 461	63.041	-0.515	54.824	1.00	17.98	2726	O PRO A 468	55.032	17.290	59.223	1.00	24.09
2674	CA THR A 461	62.842	0.254	56.179	1.00	17.58	2727	CB PRO A 468	58.442	18.647	56.967	1.00	24.08
2675	C THR A 461	62.824	-0.422	57.195	1.00	17.01	2728	CG PRO A 468	58.260	17.127	57.004	1.00	23.34
2676	O THR A 461	64.340	-1.338	55.019	1.00	17.81	2729	CD PRO A 468	55.809	18.622	60.845	1.00	28.85
2677	CB THR A 461	65.418	-0.430	55.344	1.00	16.28	2730	N ASP A 469	54.568	18.580	61.605	1.00	31.00
2678	CG1 THR A 461	64.706	-2.058	53.713	1.00	18.33	2731	CA ASP A 469	54.190	17.167	62.012	1.00	29.54
2679	CG2 THR A 461	62.820	1.569	56.197	1.00	17.91	2732	C ASP A 469	53.005	16.831	62.142	1.00	25.09
2680	N GLU A 462	62.881	2.254	57.509	1.00	18.73	2733	O ASP A 469	53.429	19.166	60.762	1.00	35.81
2681	CA GLU A 462	61.452	2.526	58.028	1.00	20.80	2734	CB ASP A 469	53.461	20.687	60.704	1.00	41.18
2682	C GLU A 462	60.651	3.247	57.389	1.00	17.17	2735	CG ASP A 469	54.229	21.361	61.442	1.00	42.60
2683	O GLU A 462	63.597	3.584	57.237	1.00	19.94	2736	OD1 ASP A 469	55.216	16.314	62.194	1.00	27.09
2684	CB GLU A 462	65.032	3.372	56.651	1.00	20.13	2737	OD2 ASP A 469	52.675	21.251	59.899	1.00	40.71
2685	CG GLU A 462	65.759	4.695	56.580	1.00	21.29	2738	N HIS A 470	55.991	14.943	62.567	1.00	29.90
2686	CD GLU A 462	65.461	5.602	57.401	1.00	22.06	2739	CA HIS A 470	54.158	14.124	61.571	1.00	27.51
2687	OE1 GLU A 462	66.629	4.885	55.702	1.00	20.07	2740	C HIS A 470	53.713	13.036	61.986	1.00	25.40
2688	OE2 GLU A 462	61.096	1.977	59.194	1.00	20.54	2741	O HIS A 470	54.351	14.933	63.968	1.00	35.53
2689	N HIS A 463	59.778	2.170	59.831	1.00	22.30	2742	CB HIS A 470	54.293	12.781	65.341	1.00	44.60
2690	CA HIS A 463	60.819	3.350	60.778	1.00	22.71	2743	CG HIS A 470	56.338	13.553	64.868	1.00	44.13
2691	C HIS A 463	60.819	3.655	61.359	1.00	23.44	2744	ND1 HIS A 470	55.239	11.999	65.896	1.00	45.27
2692	O HIS A 463	59.476	0.918	60.666	1.00	24.53	2745	CD2 HIS A 470	56.472	12.438	65.630	1.00	45.71
2693	CB HIS A 463	59.062	-0.209	59.775	1.00	26.84	2746	CE1 HIS A 470	54.101	14.443	60.279	1.00	24.01
2694	CG HIS A 463	59.954	-1.062	59.187	1.00	29.88	2747	NE2 HIS A 470	53.376	13.539	59.370	1.00	22.37
2695	ND1 HIS A 463	57.841	-0.611	59.362	1.00	28.11	2748	N VAL A 471	54.211	12.254	59.214	1.00	21.98
2696	CD2 HIS A 463	59.315	-1.954	58.450	1.00	29.51	2749	CA VAL A 471					
2697	CE1 HIS A 463						2750	C VAL A 471					

2751	O	VAL A 471	55.442	12.318	59.299	1.00	20.13	2804	CD2	LEU A 478	53.898	5.003	49.304	1.00	17.67
2752	CB	VAL A 471	53.104	14.132	57.982	1.00	21.65	2805	N	LVS A 479	51.418	2.843	53.647	1.00	20.29
2753	CG1	VAL A 471	52.190	15.365	58.015	1.00	19.93	2806	CA	LVS A 479	50.448	2.085	54.413	1.00	23.91
2754	CG2	VAL A 471	54.419	14.466	57.278	1.00	20.15	2807	C	LVS A 479	49.209	2.910	54.724	1.00	22.75
2755	N	LVS A 472	53.542	11.139	58.935	1.00	19.69	2808	O	LVS A 479	48.056	2.535	54.473	1.00	23.72
2756	CA	LVS A 472	54.244	9.876	58.649	1.00	18.37	2809	CB	LVS A 479	51.049	1.642	55.759	1.00	27.33
2757	C	LVS A 472	54.846	9.942	57.237	1.00	17.74	2810	CG	LVS A 479	50.226	0.539	56.358	1.00	32.76
2758	O	LVS A 472	54.211	10.506	56.321	1.00	17.56	2811	CD	LVS A 479	50.636	-0.179	57.602	1.00	37.03
2759	CB	LVS A 472	53.212	8.750	58.700	1.00	21.16	2812	CE	LVS A 479	52.051	-0.291	58.088	1.00	40.23
2760	CG	LVS A 472	52.495	8.535	60.043	1.00	20.15	2813	NZ	LVS A 479	52.935	-1.004	57.114	1.00	42.37
2761	CD	LVS A 472	51.529	7.341	59.924	1.00	21.24	2814	N	GLU A 480	49.388	4.126	55.242	1.00	21.40
2762	CE	LVS A 472	51.192	6.810	61.317	1.00	25.17	2815	CA	GLU A 480	48.229	4.920	55.588	1.00	22.52
2763	NZ	LVS A 472	50.187	5.690	61.273	1.00	26.92	2816	C	GLU A 480	47.449	5.378	54.364	1.00	19.27
2764	CB	LVS A 473	56.073	9.506	56.991	1.00	16.26	2817	O	GLU A 480	46.229	5.531	54.458	1.00	16.95
2765	CA	THR A 473	56.650	9.508	55.639	1.00	17.04	2818	CB	GLU A 480	48.490	6.066	56.547	1.00	25.40
2766	C	THR A 473	57.096	8.108	55.226	1.00	16.39	2819	CG	GLU A 480	49.133	7.273	55.983	1.00	28.08
2767	O	THR A 473	56.881	7.201	56.041	1.00	14.08	2820	CD	GLU A 480	49.042	8.444	56.945	1.00	30.33
2768	CB	THR A 473	57.916	10.402	55.585	1.00	17.28	2821	OE1	GLU A 480	48.009	8.573	57.618	1.00	33.89
2769	CG1	THR A 473	58.862	9.885	56.543	1.00	17.62	2822	OE2	GLU A 480	49.967	9.261	57.025	1.00	26.83
2770	CG2	THR A 473	57.590	11.827	56.000	1.00	15.72	2823	N	LEU A 481	48.091	5.482	53.220	1.00	19.95
2771	N	GLY A 474	57.706	7.921	54.044	1.00	15.36	2824	CA	LEU A 481	47.406	5.891	51.984	1.00	16.96
2772	CA	GLY A 474	57.174	5.503	53.681	1.00	17.27	2825	C	LEU A 481	46.484	4.792	51.463	1.00	17.11
2773	C	GLY A 474	55.985	5.776	53.434	1.00	15.09	2826	O	LEU A 481	45.404	5.121	50.925	1.00	15.46
2774	N	ILE A 475	57.568	4.262	53.897	1.00	18.67	2827	CB	LEU A 481	48.070	6.240	50.976	1.00	17.20
2775	N	ILE A 475	56.630	3.138	53.914	1.00	20.49	2828	CG	LEU A 481	48.070	6.823	49.640	1.00	17.62
2776	CA	ILE A 475	55.474	3.256	54.907	1.00	19.29	2829	CD1	LEU A 481	47.221	8.098	49.831	1.00	16.14
2777	C	ILE A 475	54.377	2.749	54.563	1.00	18.42	2830	CD2	LEU A 481	49.273	7.277	48.811	1.00	14.35
2778	O	ILE A 475	57.414	1.826	54.113	1.00	22.81	2831	N	GLY A 482	46.845	3.526	51.664	1.00	15.48
2779	CB	ILE A 475	56.478	0.702	53.724	1.00	24.37	2832	CA	GLY A 482	46.042	2.419	51.161	1.00	15.68
2780	CG1	ILE A 475	57.885	1.646	55.592	1.00	21.69	2833	C	GLY A 482	46.507	1.767	49.851	1.00	16.09
2781	CG2	ILE A 475	57.108	-0.682	53.618	1.00	28.52	2834	O	GLY A 482	45.908	0.771	49.461	1.00	14.56
2782	CD1	ILE A 475	55.616	3.969	56.026	1.00	17.17	2835	N	ILE A 483	47.483	2.333	49.124	1.00	15.13
2783	N	ASP A 476	54.413	4.168	56.891	1.00	17.44	2836	CA	ILE A 483	47.942	1.737	47.849	1.00	15.05
2784	CA	ASP A 476	53.387	5.060	56.185	1.00	16.48	2837	C	ILE A 483	48.385	0.301	48.077	1.00	15.90
2785	C	ASP A 476	52.197	4.895	56.429	1.00	15.25	2838	O	ILE A 483	48.723	-0.099	49.196	1.00	17.41
2786	O	ASP A 476	54.756	4.796	58.234	1.00	16.38	2839	CB	ILE A 483	49.000	2.569	47.120	1.00	14.77
2787	CB	ASP A 476	55.480	3.874	59.211	1.00	18.13	2840	CG1	ILE A 483	50.358	2.717	47.833	1.00	15.86
2788	CG	ASP A 476	55.930	4.354	60.259	1.00	17.91	2841	CG2	ILE A 483	48.429	3.967	46.809	1.00	15.27
2789	OD1	ASP A 476	53.786	6.034	55.354	1.00	16.25	2842	CD1	ILE A 483	51.356	1.531	47.671	1.00	13.17
2790	OD2	ASP A 476	52.848	6.880	54.629	1.00	16.55	2843	N	THR A 484	48.308	-0.555	47.050	1.00	15.28
2791	N	SER A 477	50.912	6.237	53.283	1.00	19.12	2844	CA	THR A 484	48.633	-1.952	47.213	1.00	15.28
2792	CA	SER A 477	53.532	8.086	53.987	1.00	15.71	2845	C	THR A 484	49.933	-2.359	46.538	1.00	15.86
2793	C	SER A 477	52.108	6.065	53.549	1.00	18.34	2846	O	THR A 484	50.410	-3.469	46.796	1.00	13.72
2794	O	SER A 477	50.912	6.237	53.283	1.00	19.12	2847	CB	THR A 484	47.549	-2.863	46.532	1.00	16.48
2795	CB	SER A 477	53.532	8.086	53.987	1.00	15.71	2848	CG1	THR A 484	47.638	-2.693	45.102	1.00	16.43
2796	OG	SER A 477	52.610	8.857	53.192	1.00	17.49	2849	CG2	THR A 484	46.150	-2.505	47.003	1.00	16.06
2797	N	LEU A 478	52.825	5.184	52.841	1.00	18.20	2850	N	THR A 485	50.443	-1.551	45.605	1.00	14.91
2798	CA	LEU A 478	52.237	4.299	51.853	1.00	17.44	2851	CA	THR A 485	51.595	-1.965	44.783	1.00	15.42
2799	C	LEU A 478	51.154	3.403	52.475	1.00	19.05	2852	C	THR A 485	52.427	-0.757	44.384	1.00	15.53
2800	O	LEU A 478	50.062	3.242	51.912	1.00	16.99	2853	O	THR A 485	51.863	0.244	43.919	1.00	15.10
2801	CB	LEU A 478	53.296	3.419	51.195	1.00	17.36	2854	CB	THR A 485	51.065	-2.655	43.513	1.00	15.83
2802	CG	LEU A 478	54.412	4.051	50.367	1.00	18.83	2855	CG1	THR A 485	50.004	-3.584	43.802	1.00	16.38
2803	CD1	LEU A 478	55.262	2.927	49.763	1.00	20.70	2856	CG2	THR A 485	52.059	-3.489	42.695	1.00	16.14

2857	N	VAL A 486	53.764	-0.790	44.555	1.00	14.94	2910	CD	GLU A 492	65.731	-4.713	33.824	1.00	16.24
2858	CA	VAL A 486	54.652	0.297	44.134	1.00	12.74	2911	OE1	GLU A 492	65.079	-5.765	33.984	1.00	15.93
2859	C	VAL A 486	55.245	0.001	42.748	1.00	14.15	2912	OE2	GLU A 492	65.871	-4.235	32.678	1.00	16.98
2860	O	VAL A 486	55.788	-1.134	42.601	1.00	14.85	2913	N	GLU A 493	70.400	-1.716	35.653	1.00	17.89
2861	CB	VAL A 486	55.857	0.483	45.082	1.00	14.01	2914	CA	GLU A 493	71.592	-0.901	35.413	1.00	18.19
2862	CG1	VAL A 486	56.783	1.610	44.531	1.00	12.76	2915	C	GLU A 493	71.592	-0.092	34.107	1.00	17.67
2863	CG2	VAL A 486	55.303	0.961	46.438	1.00	15.43	2916	O	GLU A 493	71.592	-0.640	33.012	1.00	15.24
2864	N	GLN A 487	55.159	0.899	41.798	1.00	12.39	2917	CB	GLU A 493	72.869	-1.773	35.447	1.00	18.34
2865	CA	GLN A 487	55.823	0.699	40.507	1.00	13.69	2918	CG	GLU A 493	74.173	-1.020	35.230	1.00	18.92
2866	C	GLN A 487	57.124	1.507	40.520	1.00	14.02	2919	CD	GLU A 493	74.742	-0.344	36.455	1.00	19.23
2867	O	GLN A 487	57.008	2.717	40.530	1.00	15.37	2920	OE1	GLU A 493	75.796	0.334	36.325	1.00	17.41
2868	CB	GLN A 487	54.975	1.132	39.304	1.00	14.53	2921	OE2	GLU A 493	74.095	-0.479	37.541	1.00	19.62
2869	CG	GLN A 487	55.555	0.810	37.899	1.00	14.85	2922	N	PHE A 494	71.755	1.230	34.238	1.00	15.08
2870	CD	GLN A 487	54.658	1.489	36.844	1.00	15.25	2923	CA	PHE A 494	71.716	2.064	33.051	1.00	17.22
2871	OE1	GLN A 487	53.542	0.999	36.600	1.00	12.63	2924	C	PHE A 494	73.040	2.834	32.904	1.00	17.93
2872	NE2	GLN A 487	55.086	2.600	36.263	1.00	14.69	2925	O	PHE A 494	73.846	2.871	33.840	1.00	17.61
2873	N	LEU A 488	58.291	0.856	40.520	1.00	13.77	2926	CB	PHE A 494	70.494	2.985	33.079	1.00	15.05
2874	CA	LEU A 488	59.537	1.560	40.518	1.00	15.79	2927	CG	PHE A 494	70.209	3.732	34.347	1.00	13.69
2875	C	LEU A 488	60.035	1.987	39.152	1.00	15.05	2928	CD1	PHE A 494	69.309	3.238	35.283	1.00	13.97
2876	O	LEU A 488	60.073	1.122	38.294	1.00	15.87	2929	CD2	PHE A 494	70.814	4.964	34.603	1.00	14.09
2877	CB	LEU A 488	60.695	0.684	41.146	1.00	14.51	2930	CE1	PHE A 494	69.008	3.927	36.442	1.00	13.34
2878	CG	LEU A 488	60.575	0.236	42.618	1.00	16.06	2931	CE2	PHE A 494	70.548	5.662	35.766	1.00	13.82
2879	CD1	LEU A 488	61.575	-0.885	42.971	1.00	15.85	2932	CZ	PHE A 494	69.650	5.128	36.706	1.00	14.68
2880	CD2	LEU A 488	60.742	1.336	43.642	1.00	11.74	2933	N	ASN A 495	73.262	3.489	31.758	1.00	17.56
2881	N	GLN A 489	60.487	3.246	39.045	1.00	15.31	2934	CA	ASN A 495	74.549	4.074	31.443	1.00	19.21
2882	CA	GLN A 489	61.188	3.679	37.812	1.00	14.87	2935	C	ASN A 495	74.759	5.505	31.926	1.00	18.67
2883	C	GLN A 489	62.425	2.807	37.665	1.00	14.33	2936	O	ASN A 495	75.915	5.887	32.059	1.00	17.87
2884	O	GLN A 489	62.859	2.155	38.606	1.00	14.60	2937	CB	ASN A 495	74.850	4.084	29.931	1.00	17.20
2885	CB	GLN A 489	61.403	5.188	37.805	1.00	15.88	2938	CG	ASN A 495	76.266	4.473	29.570	1.00	20.20
2886	CD	GLN A 489	60.080	5.982	37.617	1.00	16.42	2939	OD1	ASN A 495	77.257	3.802	29.891	1.00	18.77
2887	CG	GLN A 489	60.312	7.400	37.152	1.00	16.75	2940	ND2	ASN A 495	76.482	5.618	28.938	1.00	19.57
2888	OE1	GLN A 489	60.684	7.691	35.982	1.00	19.64	2941	N	SER A 496	73.715	6.299	32.041	1.00	17.54
2889	NE2	GLN A 489	60.177	8.368	38.027	1.00	14.55	2942	CA	SER A 496	73.827	7.723	32.297	1.00	17.54
2890	N	PRO A 490	63.045	2.689	36.494	1.00	14.20	2943	C	SER A 496	74.342	8.127	33.652	1.00	18.68
2891	CA	PRO A 490	64.089	1.703	36.225	1.00	13.53	2944	O	SER A 496	74.638	9.331	33.798	1.00	18.94
2892	C	PRO A 490	65.155	1.438	37.241	1.00	14.81	2945	CB	SER A 496	72.487	8.433	32.001	1.00	19.07
2893	O	PRO A 490	65.895	2.388	37.605	1.00	15.34	2946	OG	SER A 496	71.377	7.889	32.711	1.00	17.68
2894	CB	PRO A 490	64.707	2.269	34.906	1.00	13.82	2947	N	ILE A 497	74.441	7.273	34.670	1.00	16.74
2895	CG	PRO A 490	63.479	2.776	34.197	1.00	15.17	2948	CA	ILE A 497	75.071	7.777	35.908	1.00	17.05
2896	CD	PRO A 490	62.691	3.502	35.299	1.00	11.82	2949	C	ILE A 497	76.434	7.104	36.029	1.00	17.86
2897	N	VAL A 491	65.280	0.210	37.709	1.00	14.57	2950	O	ILE A 497	76.528	5.880	35.928	1.00	16.60
2898	CA	VAL A 491	66.362	-0.156	38.655	1.00	16.33	2951	CB	ILE A 497	74.203	7.473	37.156	1.00	18.85
2899	C	VAL A 491	67.293	-1.160	37.970	1.00	17.32	2952	CG1	ILE A 497	72.950	8.366	37.145	1.00	18.39
2900	O	VAL A 491	68.202	-1.714	38.584	1.00	17.98	2953	CG2	ILE A 497	75.033	7.586	38.435	1.00	16.11
2901	CB	VAL A 491	65.792	-0.718	39.976	1.00	15.46	2954	CG1	ILE A 497	71.845	8.001	38.145	1.00	18.90
2902	CG1	VAL A 491	64.974	0.369	40.708	1.00	13.55	2955	N	ASP A 498	77.478	7.888	36.227	1.00	18.34
2903	CG2	VAL A 491	64.915	-1.944	39.688	1.00	14.62	2956	CA	ASP A 498	78.806	7.346	36.522	1.00	19.14
2904	N	GLU A 492	67.092	-1.504	36.697	1.00	18.44	2957	C	ASP A 498	78.770	6.898	37.971	1.00	17.01
2905	CA	GLU A 492	68.031	-2.245	35.863	1.00	16.40	2958	O	ASP A 498	78.609	7.762	38.858	1.00	15.12
2906	C	GLU A 492	69.156	-1.271	35.451	1.00	17.63	2959	CB	ASP A 498	79.861	8.458	36.364	1.00	21.90
2907	O	GLU A 492	68.937	-0.141	34.964	1.00	15.32	2960	CG	ASP A 498	81.295	8.069	36.759	1.00	24.10
2908	CB	GLU A 492	67.459	-2.927	34.598	1.00	15.59	2961	OD1	ASP A 498	82.155	8.832	36.229	1.00	23.49
2909	CG	GLU A 492	66.412	-4.003	34.981	1.00	16.27	2962	OD2	ASP A 498	81.615	7.096	37.480	1.00	19.87

2963	N	GLU A 499	79.011	5.646	38.280	1.00	16.55	3016	CD1 TYR A 505	67.241	13.027	40.115	1.00	17.54
2964	CA	GLU A 499	78.977	5.108	39.632	1.00	19.92	3017	CD2 TYR A 505	67.023	13.226	37.730	1.00	16.46
2965	C	GLU A 499	79.988	5.691	40.614	1.00	21.17	3018	CE1 TYR A 505	65.931	12.559	40.199	1.00	16.03
2966	O	GLU A 499	79.775	5.543	41.836	1.00	20.23	3019	CE2 TYR A 505	65.697	12.777	37.831	1.00	16.62
2967	CB	GLU A 499	79.090	3.565	39.610	1.00	18.52	3020	CZ TYR A 505	65.163	12.442	39.058	1.00	17.37
2968	CG	GLU A 499	77.783	3.044	38.948	1.00	17.11	3021	OH TYR A 505	63.859	11.975	39.132	1.00	16.33
2969	CD	GLU A 499	77.715	1.561	38.901	1.00	19.30	3022	N ASN A 506	69.117	10.864	37.112	1.00	19.02
2970	OE1	GLU A 499	78.782	0.866	38.946	1.00	18.97	3023	CA ASN A 506	68.525	10.394	35.854	1.00	17.54
2971	OE2	GLU A 499	76.609	0.973	38.775	1.00	18.01	3024	C ASN A 506	67.354	9.433	36.132	1.00	16.94
2972	N	THR A 500	81.008	6.404	40.126	1.00	20.80	3025	O ASN A 506	67.448	8.585	37.023	1.00	15.04
2973	CA	THR A 500	81.940	7.053	41.057	1.00	23.34	3026	CB ASN A 506	69.538	9.697	34.935	1.00	17.11
2974	C	THR A 500	81.372	8.400	41.497	1.00	24.20	3027	CG ASN A 506	69.102	9.692	33.481	1.00	19.56
2975	O	THR A 500	82.015	9.077	42.287	1.00	24.37	3028	OD1 ASN A 506	68.263	8.880	33.019	1.00	18.08
2976	CB	THR A 500	83.342	7.317	40.473	1.00	21.92	3029	ND2 ASN A 506	69.679	10.641	32.729	1.00	18.09
2977	OG1	THR A 500	83.230	8.244	39.379	1.00	20.76	3030	N TRP A 507	66.363	9.479	35.216	1.00	14.78
2978	CG2	THR A 500	84.023	6.044	39.986	1.00	22.58	3031	CA TRP A 507	65.263	8.515	35.282	1.00	14.79
2979	N	GLN A 501	80.313	8.895	40.895	1.00	26.63	3032	C TRP A 507	65.716	7.096	34.995	1.00	14.58
2980	CA	GLN A 501	79.580	10.111	41.217	1.00	29.35	3033	O TRP A 507	65.101	6.151	35.466	1.00	12.62
2981	C	GLN A 501	78.081	9.780	41.293	1.00	29.18	3034	CB TRP A 507	64.189	8.879	34.236	1.00	13.89
2982	O	GLN A 501	77.286	10.114	40.421	1.00	28.10	3035	CG TRP A 507	63.208	9.944	34.647	1.00	13.96
2983	CB	GLN A 501	79.695	11.145	40.089	1.00	32.33	3036	CD1 TRP A 507	63.021	10.504	35.878	1.00	13.86
2984	CG	GLN A 501	81.113	11.471	39.637	1.00	36.70	3037	CD2 TRP A 507	62.268	10.598	33.765	1.00	13.76
2985	CD	GLN A 501	81.850	12.239	40.710	1.00	41.32	3038	NE1 TRP A 507	62.035	11.509	35.797	1.00	14.63
2986	OE1	GLN A 501	81.235	12.619	41.723	1.00	43.52	3039	CE2 TRP A 507	61.572	11.557	34.520	1.00	14.09
2987	NE2	GLN A 501	83.153	12.497	40.515	1.00	44.21	3040	CE3 TRP A 507	62.006	10.488	32.396	1.00	14.36
2988	N	PRO A 502	77.652	9.030	42.297	1.00	29.53	3041	CZ2 TRP A 507	60.623	12.410	33.943	1.00	15.35
2989	CA	PRO A 502	76.292	8.507	42.359	1.00	28.54	3042	CZ3 TRP A 507	61.039	11.314	31.837	1.00	16.79
2990	C	PRO A 502	75.175	9.471	42.670	1.00	28.87	3043	CH2 TRP A 507	60.359	12.283	32.620	1.00	14.29
2991	O	PRO A 502	74.004	9.050	42.701	1.00	30.15	3044	N GLY A 508	66.779	6.933	34.176	1.00	14.06
2992	CB	PRO A 502	76.406	7.392	43.399	1.00	26.18	3045	CA GLY A 508	67.280	5.621	33.845	1.00	14.97
2993	CD	PRO A 502	77.510	7.853	44.309	1.00	27.23	3046	C GLY A 508	66.688	4.906	32.664	1.00	14.99
2994	CD	PRO A 502	78.477	8.622	43.471	1.00	27.08	3047	O GLY A 508	66.794	3.661	32.610	1.00	13.65
2995	N	ASP A 503	75.432	10.751	42.881	1.00	28.94	3048	N TYR A 509	66.161	5.623	31.664	1.00	15.66
2996	CA	ASP A 503	74.380	11.709	43.179	1.00	29.84	3049	CA TYR A 509	65.673	5.037	30.419	1.00	16.40
2997	C	ASP A 503	73.930	12.521	41.976	1.00	28.92	3050	C TYR A 509	66.771	4.746	29.389	1.00	16.91
2998	O	ASP A 503	73.125	13.446	42.132	1.00	30.62	3051	O TYR A 509	66.436	4.451	28.241	1.00	16.03
2999	CB	ASP A 503	74.783	12.642	44.344	1.00	29.97	3052	CB TYR A 509	64.471	5.812	29.758	1.00	14.79
3000	CG	ASP A 503	74.845	11.877	45.654	1.00	31.52	3053	CG TYR A 509	63.288	5.731	30.729	1.00	17.63
3001	OD1	ASP A 503	74.016	10.975	45.912	1.00	29.14	3054	CD1 TYR A 509	62.469	4.608	30.816	1.00	15.29
3002	OD2	ASP A 503	75.783	12.160	46.439	1.00	33.43	3055	CD2 TYR A 509	63.037	6.779	31.616	1.00	17.85
3003	N	THR A 504	74.384	12.204	40.790	1.00	28.14	3056	CE1 TYR A 509	61.434	4.549	31.726	1.00	14.88
3004	CA	THR A 504	73.894	12.795	39.547	1.00	28.02	3057	CE2 TYR A 509	62.012	6.715	32.540	1.00	17.47
3005	C	THR A 504	72.464	12.303	39.332	1.00	25.44	3058	CZ TYR A 509	61.210	5.585	32.587	1.00	18.26
3006	O	THR A 504	72.090	11.307	39.988	1.00	26.41	3059	OH TYR A 509	60.204	5.532	33.541	1.00	18.82
3007	CB	THR A 504	74.817	12.287	38.421	1.00	30.26	3060	N ASP A 510	68.021	4.495	29.735	1.00	16.31
3008	OG1	THR A 504	74.365	12.697	37.137	1.00	34.86	3061	CA ASP A 510	69.142	4.129	28.870	1.00	18.35
3009	CG2	THR A 504	74.853	10.784	38.452	1.00	32.35	3062	C ASP A 510	69.891	2.912	29.392	1.00	17.34
3010	N	TYR A 505	71.617	12.976	38.574	1.00	22.48	3063	O ASP A 510	71.041	2.945	29.873	1.00	20.99
3011	CA	TYR A 505	70.198	12.564	38.498	1.00	20.51	3064	CB ASP A 510	70.120	5.322	28.723	1.00	19.25
3012	C	TYR A 505	69.839	11.991	37.135	1.00	20.40	3065	CG ASP A 510	70.746	5.804	30.000	1.00	21.01
3013	O	TYR A 505	70.037	12.679	36.103	1.00	19.81	3066	OD1 ASP A 510	70.057	5.942	31.032	1.00	21.87
3014	CB	TYR A 505	69.281	13.777	38.795	1.00	19.30	3067	OD2 ASP A 510	71.991	6.068	30.056	1.00	23.52
3015	CG	TYR A 505	67.814	13.347	38.862	1.00	19.19	3068	N PRO A 511	69.294	1.752	29.370	1.00	16.56

3069	CA	PRO A 511	69.789	0.507	29.915	1.00	17.26
3070	C	PRO A 511	71.112	0.019	29.272	1.00	17.06
3071	O	PRO A 511	71.327	0.259	28.077	1.00	16.16
3072	CB	PRO A 511	68.730	-0.564	29.675	1.00	16.53
3073	CG	PRO A 511	67.898	-0.001	28.531	1.00	17.61
3074	CD	PRO A 511	67.914	1.498	28.752	1.00	17.12
3075	N	ARG A 512	71.925	-0.624	30.102	1.00	16.69
3076	CA	ARG A 512	73.212	-1.174	29.634	1.00	16.56
3077	C	ARG A 512	73.392	-2.618	30.065	1.00	16.11
3078	O	ARG A 512	73.824	-3.472	29.278	1.00	16.43
3079	CB	ARG A 512	74.394	-0.275	30.088	1.00	18.15
3080	CG	ARG A 512	75.778	-0.703	29.616	1.00	18.63
3081	CD	ARG A 512	76.929	0.127	30.219	1.00	19.47
3082	NE	ARG A 512	77.011	-0.045	31.687	1.00	20.90
3083	CZ	ARG A 512	77.354	0.937	32.563	1.00	20.85
3084	NH1	ARG A 512	77.328	0.708	33.877	1.00	20.82
3085	NH2	ARG A 512	77.653	2.184	32.233	1.00	19.17
3086	N	ASN A 513	73.175	-2.970	31.326	1.00	15.21
3087	CA	ASN A 513	73.323	-4.307	31.896	1.00	14.14
3088	C	ASN A 513	71.957	-4.696	32.471	1.00	15.83
3089	O	ASN A 513	71.562	-4.414	33.623	1.00	14.75
3090	CB	ASN A 513	74.425	-4.304	32.991	1.00	13.68
3091	CG	ASN A 513	75.722	-3.670	32.503	1.00	15.65
3092	OD1	ASN A 513	75.960	-2.463	32.702	1.00	13.93
3093	ND2	ASN A 513	76.592	-4.443	31.817	1.00	13.93
3094	N	TYR A 514	71.137	-5.398	31.687	1.00	16.49
3095	CA	TYR A 514	69.742	-5.666	32.068	1.00	17.77
3096	C	TYR A 514	69.496	-6.572	33.280	1.00	18.89
3097	O	TYR A 514	68.398	-6.564	33.865	1.00	16.26
3098	CB	TYR A 514	69.017	-6.266	30.861	1.00	18.16
3099	CG	TYR A 514	68.726	-5.341	29.689	1.00	18.97
3100	CD1	TYR A 514	67.565	-4.560	29.672	1.00	18.42
3101	CD2	TYR A 514	69.604	-5.279	28.597	1.00	19.59
3102	CE1	TYR A 514	67.289	-3.734	28.595	1.00	18.29
3103	CE2	TYR A 514	69.328	-4.444	27.514	1.00	19.38
3104	CZ	TYR A 514	68.167	-3.696	27.521	1.00	19.34
3105	OH	TYR A 514	67.857	-2.887	26.450	1.00	22.29
3106	N	ASN A 515	70.493	-7.389	33.643	1.00	17.63
3107	CA	ASN A 515	70.280	-8.339	34.745	1.00	17.34
3108	C	ASN A 515	70.978	-7.906	36.018	1.00	17.54
3109	O	ASN A 515	71.187	-8.752	36.913	1.00	18.12
3110	CB	ASN A 515	70.786	-9.703	34.185	1.00	16.85
3111	CG	ASN A 515	69.974	-10.095	32.944	1.00	18.64
3112	OD1	ASN A 515	70.465	-10.350	31.826	1.00	21.03
3113	ND2	ASN A 515	68.680	-10.119	33.147	1.00	11.82
3114	N	VAL A 516	71.402	-6.661	36.141	1.00	14.31
3115	CA	VAL A 516	72.083	-6.138	37.344	1.00	15.74
3116	C	VAL A 516	71.301	-4.960	37.911	1.00	16.74
3117	O	VAL A 516	70.892	-4.053	37.176	1.00	16.35
3118	CB	VAL A 516	73.478	-5.606	36.838	1.00	16.38
3119	CG1	VAL A 516	74.289	-4.915	37.924	1.00	15.90
3120	CG2	VAL A 516	74.293	-6.720	36.163	1.00	15.48
3121	N	PRO A 517	71.121	-4.832	39.223	1.00	17.59
3122	CA	PRO A 517	69.789	0.507	29.915	1.00	17.26
3123	C	PRO A 517	71.112	0.019	29.272	1.00	17.06
3124	O	PRO A 517	71.327	0.259	28.077	1.00	16.16
3125	CB	PRO A 517	68.730	-0.564	29.675	1.00	16.53
3126	CG	PRO A 517	67.898	-0.001	28.531	1.00	17.61
3127	CD	PRO A 517	67.914	1.498	28.752	1.00	17.12
3128	N	GLU A 518	71.925	-0.624	30.102	1.00	16.69
3129	CA	GLU A 518	73.212	-1.174	29.634	1.00	16.56
3130	C	GLU A 518	73.392	-2.618	30.065	1.00	16.11
3131	O	GLU A 518	73.824	-3.472	29.278	1.00	16.43
3132	CB	GLU A 518	74.394	-0.275	30.088	1.00	18.15
3133	CG	GLU A 518	75.778	-0.703	29.616	1.00	18.63
3134	CD	GLU A 518	76.929	0.127	30.219	1.00	19.47
3135	OE1	GLU A 518	77.011	-0.045	31.687	1.00	20.90
3136	OE2	GLU A 518	77.354	0.937	32.563	1.00	20.85
3137	N	GLY A 519	77.328	0.708	33.877	1.00	20.82
3138	CA	GLY A 519	77.653	2.184	32.233	1.00	19.17
3139	C	GLY A 519	73.175	-2.970	31.326	1.00	15.21
3140	O	GLY A 519	73.323	-4.307	31.896	1.00	14.14
3141	N	ALA A 520	71.957	-4.696	32.471	1.00	15.83
3142	CA	ALA A 520	71.562	-4.414	33.623	1.00	14.75
3143	C	ALA A 520	74.425	-4.304	32.991	1.00	13.68
3144	O	ALA A 520	75.722	-3.670	32.503	1.00	15.65
3145	CB	ALA A 520	75.960	-2.463	32.702	1.00	13.93
3146	N	TYR A 521	76.592	-4.443	31.817	1.00	13.93
3147	CA	TYR A 521	71.137	-5.398	31.687	1.00	16.49
3148	C	TYR A 521	69.742	-5.666	32.068	1.00	17.77
3149	O	TYR A 521	69.496	-6.572	33.280	1.00	18.89
3150	CB	TYR A 521	68.398	-6.564	33.865	1.00	16.26
3151	CG	TYR A 521	69.017	-6.266	30.861	1.00	18.16
3152	CD1	TYR A 521	68.726	-5.341	29.689	1.00	18.97
3153	CD2	TYR A 521	67.565	-4.560	29.672	1.00	18.42
3154	CE1	TYR A 521	69.604	-5.279	28.597	1.00	19.59
3155	CE2	TYR A 521	67.289	-3.734	28.595	1.00	18.29
3156	CZ	TYR A 521	69.328	-4.444	27.514	1.00	19.38
3157	OH	TYR A 521	68.167	-3.696	27.521	1.00	19.34
3158	N	ALA A 522	70.493	-7.389	33.643	1.00	17.63
3159	CA	ALA A 522	70.280	-8.339	34.745	1.00	17.34
3160	C	ALA A 522	70.978	-7.906	36.018	1.00	17.54
3161	O	ALA A 522	71.187	-8.752	36.913	1.00	18.12
3162	CB	ALA A 522	70.786	-9.703	34.185	1.00	16.85
3163	N	THR A 523	69.974	-10.095	32.944	1.00	18.64
3164	CA	THR A 523	70.465	-10.350	31.826	1.00	21.03
3165	C	THR A 523	68.680	-10.119	33.147	1.00	11.82
3166	O	THR A 523	71.402	-6.661	36.141	1.00	14.31
3167	CB	THR A 523	72.083	-6.138	37.344	1.00	15.74
3168	OG1	THR A 523	71.301	-4.960	37.911	1.00	16.74
3169	CG2	THR A 523	70.892	-4.053	37.176	1.00	16.35
3170	N	THR A 524	73.478	-5.606	36.838	1.00	16.38
3171	CA	THR A 524	74.289	-4.915	37.924	1.00	15.90
3172	C	THR A 524	74.293	-6.720	36.163	1.00	15.48
3173	O	THR A 524	71.121	-4.832	39.223	1.00	17.59
3174	CB	THR A 524	69.789	0.507	29.915	1.00	17.26
3175	C	THR A 524	71.112	0.019	29.272	1.00	17.06
3176	O	THR A 524	71.327	0.259	28.077	1.00	16.16
3177	CB	THR A 524	68.730	-0.564	29.675	1.00	16.53
3178	CG	THR A 524	67.898	-0.001	28.531	1.00	17.61
3179	CD	THR A 524	67.914	1.498	28.752	1.00	17.12
3180	N	GLU A 518	71.925	-0.624	30.102	1.00	16.69
3181	CA	GLU A 518	73.212	-1.174	29.634	1.00	16.56
3182	C	GLU A 518	73.392	-2.618	30.065	1.00	16.11
3183	O	GLU A 518	73.824	-3.472	29.278	1.00	16.43
3184	CB	GLU A 518	74.394	-0.275	30.088	1.00	18.15
3185	CG	GLU A 518	75.778	-0.703	29.616	1.00	18.63
3186	CD	GLU A 518	76.929	0.127	30.219	1.00	19.47
3187	OE1	GLU A 518	77.011	-0.045	31.687	1.00	20.90
3188	OE2	GLU A 518	77.354	0.937	32.563	1.00	20.85
3189	N	GLY A 519	77.328	0.708	33.877	1.00	20.82
3190	CA	GLY A 519	77.653	2.184	32.233	1.00	19.17
3191	C	GLY A 519	73.175	-2.970	31.326	1.00	15.21
3192	O	GLY A 519	73.323	-4.307	31.896	1.00	14.14
3193	N	ALA A 520	71.957	-4.696	32.471	1.00	15.83
3194	CA	ALA A 520	71.562	-4.414	33.623	1.00	14.75
3195	C	ALA A 520	74.425	-4.304	32.991	1.00	13.68
3196	O	ALA A 520	75.722	-3.670	32.503	1.00	15.65
3197	CB	ALA A 520	75.960	-2.463	32.702	1.00	13.93
3198	N	TYR A 521	76.592	-4.443	31.817	1.00	13.93
3199	CA	TYR A 521	71.137	-5.398	31.687	1.00	16.49
3200	C	TYR A 521	69.742	-5.666	32.068	1.00	17.77
3201	O	TYR A 521	69.496	-6.572	33.280	1.00	18.89
3202	CB	TYR A 521	68.398	-6.564	33.865	1.00	16.26
3203	CG	TYR A 521	69.017	-6.266	30.861	1.00	18.16
3204	CD1	TYR A 521	68.726	-5.341	29.689	1.00	18.97
3205	CD2	TYR A 521	67.565	-4.560	29.672	1.00	18.42
3206	CE1	TYR A 521	69.604	-5.279	28.597	1.00	19.59
3207	CE2	TYR A 521	67.289	-3.734	28.595	1.00	18.29
3208	CZ	TYR A 521	69.328	-4.444	27.514	1.00	19.38
3209	OH	TYR A 521	68.167	-3.696	27.521	1.00	19.34
3210	N	ALA A 522	70.493	-7.389	33.643	1.00	17.63
3211	CA	ALA A 522	70.280	-8.339	34.745	1.00	17.34
3212	C	ALA A 522	70.978	-7.906	36.018	1.00	17.54
3213	O	ALA A 522	71.187	-8.752	36.913	1.00	18.12
3214	CB	ALA A 522	70.786	-9.703	34.185	1.00	16.85
3215	N	THR A 523	69.974	-10.095	32.944	1.00	18.64
3216	CA	THR A 523	70.465	-10.350	31.826	1.00	21.03
3217	C	THR A 523	68.680	-10.119	33.147	1.00	11.82
3218	O	THR A 523	71.402	-6.661	36.141		

3175	OG1	THR A 524	80.598	0.447	47.315	1.00	18.09	3228	N	THR A 532	71.717	-7.408	47.426	1.00	16.30
3176	CG2	THR A 524	79.009	-0.895	48.485	1.00	17.48	3229	CA	THR A 532	71.120	-7.596	48.745	1.00	17.14
3177	N	PRO A 525	78.671	0.941	44.975	1.00	16.83	3230	C	THR A 532	70.203	-6.408	49.093	1.00	16.96
3178	CA	PRO A 525	78.667	0.231	43.696	1.00	16.43	3231	O	THR A 532	69.122	-6.670	49.634	1.00	17.94
3179	C	PRO A 525	79.532	-1.019	43.697	1.00	17.20	3232	CB	THR A 532	72.202	-7.696	49.838	1.00	18.30
3180	O	PRO A 525	79.479	-1.868	42.773	1.00	16.05	3233	OG1	THR A 532	73.048	-8.840	49.519	1.00	17.90
3181	CB	PRO A 525	79.261	1.241	42.734	1.00	17.75	3234	CG2	THR A 532	71.578	-7.989	51.205	1.00	15.71
3182	CG	PRO A 525	80.236	2.061	43.551	1.00	17.07	3235	N	GLU A 533	70.608	-5.180	48.808	1.00	13.67
3183	CD	PRO A 525	79.581	2.153	44.935	1.00	16.46	3236	CA	GLU A 533	69.821	-3.993	49.110	1.00	15.12
3184	N	GLU A 526	80.334	-1.296	44.754	1.00	17.68	3237	C	GLU A 533	68.532	-3.891	48.317	1.00	16.63
3185	CA	GLU A 526	81.242	-2.413	44.797	1.00	15.57	3238	O	GLU A 533	67.551	-3.400	48.903	1.00	14.08
3186	C	GLU A 526	80.552	-3.755	45.025	1.00	18.65	3239	CB	GLU A 533	70.707	-2.740	49.008	1.00	16.01
3187	O	GLU A 526	79.678	-3.828	45.910	1.00	17.57	3240	CG	GLU A 533	71.882	-2.653	50.183	1.00	17.57
3188	CB	GLU A 526	82.241	-2.286	45.993	1.00	18.74	3241	CD	GLU A 533	72.716	-1.580	50.093	1.00	19.20
3189	CG	GLU A 526	83.196	-1.098	45.920	1.00	17.93	3242	OE1	GLU A 533	73.811	-1.717	50.714	1.00	21.48
3190	CD	GLU A 526	84.240	-1.354	44.831	1.00	20.14	3243	OE2	GLU A 533	72.475	-0.536	49.428	1.00	20.43
3191	OE1	GLU A 526	84.455	-2.518	44.447	1.00	18.35	3244	N	LEU A 534	68.465	-4.294	47.052	1.00	14.75
3192	OE2	GLU A 526	84.830	-0.361	44.367	1.00	20.55	3245	CA	LEU A 534	67.179	-4.230	46.320	1.00	14.76
3193	N	GLY A 527	80.932	-4.816	44.303	1.00	16.41	3246	C	LEU A 534	66.255	-5.331	46.838	1.00	13.97
3194	CA	GLY A 527	80.349	-6.100	44.587	1.00	18.62	3247	O	LEU A 534	65.040	-5.162	46.998	1.00	13.22
3195	C	GLY A 527	78.868	-6.310	44.654	1.00	19.21	3248	CB	LEU A 534	67.451	-4.277	44.804	1.00	11.25
3196	O	GLY A 527	78.114	-5.715	43.903	1.00	19.86	3249	CG	LEU A 534	66.205	-4.408	43.904	1.00	13.31
3197	N	THR A 528	78.364	-7.119	45.605	1.00	20.27	3250	CD1	LEU A 534	65.165	-3.291	44.168	1.00	10.17
3198	CA	THR A 528	76.950	-7.510	45.574	1.00	18.39	3251	CD2	LEU A 534	66.721	-4.308	42.454	1.00	10.59
3199	C	THR A 528	76.092	-6.707	46.515	1.00	19.42	3252	N	LYS A 535	66.805	-6.516	47.087	1.00	13.87
3200	O	THR A 528	74.938	-7.063	46.774	1.00	18.50	3253	CA	LYS A 535	66.086	-7.618	47.715	1.00	15.88
3201	CB	THR A 528	76.855	-9.024	45.904	1.00	18.15	3254	C	LYS A 535	65.530	-7.196	49.082	1.00	16.79
3202	OG1	THR A 528	77.414	-9.233	47.211	1.00	20.44	3255	O	LYS A 535	64.377	-7.547	49.376	1.00	17.52
3203	CG2	THR A 528	77.688	-9.855	44.941	1.00	17.77	3256	CB	LYS A 535	66.887	-8.917	47.860	1.00	15.40
3204	N	ALA A 529	76.662	-5.642	47.063	1.00	18.16	3257	CG	LYS A 535	67.402	-9.601	46.617	1.00	18.60
3205	CA	ALA A 529	75.933	-4.712	47.906	1.00	18.05	3258	CD	LYS A 535	68.119	-10.918	46.903	1.00	17.82
3206	C	ALA A 529	74.630	-4.330	47.203	1.00	18.52	3259	CE	LYS A 535	68.558	-11.541	45.575	1.00	18.33
3207	O	ALA A 529	73.580	-4.348	47.859	1.00	16.31	3260	NZ	LYS A 535	69.546	-12.644	45.766	1.00	16.36
3208	CB	ALA A 529	76.703	-3.413	48.157	1.00	18.09	3261	N	GLN A 536	66.207	-6.389	49.915	1.00	16.15
3209	N	ARG A 530	74.624	-4.063	45.907	1.00	17.37	3262	CA	GLN A 536	65.663	-5.931	51.188	1.00	17.43
3210	CA	ARG A 530	73.422	-3.669	45.184	1.00	16.22	3263	C	GLN A 536	64.484	-4.948	51.011	1.00	15.85
3211	C	ARG A 530	72.334	-4.739	45.116	1.00	16.28	3264	O	GLN A 536	63.556	-4.932	51.829	1.00	13.29
3212	O	ARG A 530	71.148	-4.377	45.045	1.00	15.45	3265	CB	GLN A 536	66.735	-5.260	52.068	1.00	16.73
3213	CB	ARG A 530	73.783	-3.225	43.762	1.00	15.05	3266	CG	GLN A 536	67.783	-6.230	52.583	1.00	20.31
3214	CG	ARG A 530	74.440	-4.346	42.940	1.00	16.74	3267	CD	GLN A 536	68.982	-5.556	53.221	1.00	22.94
3215	CD	ARG A 530	74.961	-3.751	41.630	1.00	14.90	3268	OE1	GLN A 536	69.836	-4.925	52.614	1.00	21.17
3216	NE	ARG A 530	76.197	-2.937	41.763	1.00	15.63	3269	NE2	GLN A 536	69.036	-5.681	54.536	1.00	25.61
3217	CZ	ARG A 530	76.515	-2.064	40.802	1.00	15.30	3270	N	LEU A 537	64.505	-4.105	49.992	1.00	16.38
3218	NH1	ARG A 530	77.670	-1.407	40.853	1.00	17.75	3271	CA	LEU A 537	63.425	-3.174	49.650	1.00	16.04
3219	NH2	ARG A 530	75.706	-1.836	39.773	1.00	12.09	3272	C	LEU A 537	62.179	-4.051	49.336	1.00	17.04
3220	N	ILE A 531	72.700	-6.005	45.108	1.00	14.54	3273	O	LEU A 537	61.080	-3.702	49.797	1.00	16.16
3221	CA	ILE A 531	71.804	-7.113	45.021	1.00	17.37	3274	CB	LEU A 537	63.756	-2.314	48.435	1.00	17.59
3222	C	ILE A 531	71.001	-7.347	46.318	1.00	18.65	3275	CG	LEU A 537	62.757	-1.314	47.829	1.00	15.05
3223	O	ILE A 531	69.754	-7.487	46.311	1.00	14.76	3276	CD1	LEU A 537	63.348	-0.200	46.975	1.00	16.00
3224	CB	ILE A 531	72.556	-8.391	44.601	1.00	17.38	3277	CD2	LEU A 537	61.771	-2.134	46.970	1.00	15.65
3225	CG1	ILE A 531	73.146	-8.298	43.182	1.00	17.59	3278	N	ILE A 538	62.361	-5.013	48.468	1.00	16.09
3226	CG2	ILE A 531	71.624	-9.601	44.601	1.00	16.93	3279	CA	ILE A 538	61.288	-5.922	48.067	1.00	16.51
3227	CD1	ILE A 531	73.965	-9.553	42.804	1.00	16.77	3280	C	ILE A 538	60.701	-6.677	49.245	1.00	17.89

3281	O	ILE A 538	59.479	-6.811	49.400	1.00	16.47	3334	CD	GLN A 544	54.552	-3.697	57.224	1.00	37.02
3282	CB	ILE A 538	61.777	-6.836	46.920	1.00	16.94	3335	OE1	GLN A 544	53.442	-3.372	57.648	1.00	39.96
3283	CG1	ILE A 538	62.083	-5.982	45.686	1.00	14.36	3336	NE2	GLN A 544	55.388	-4.465	57.921	1.00	38.54
3284	CG2	ILE A 538	60.667	-7.886	46.675	1.00	17.13	3337	N	ARG A 545	52.376	-6.121	53.023	1.00	24.22
3285	CD1	ILE A 538	62.805	-6.628	44.509	1.00	13.95	3338	CA	ARG A 545	51.393	-6.420	51.983	1.00	26.56
3286	N	GLN A 539	61.538	-7.186	50.141	1.00	16.57	3339	C	ARG A 545	51.405	-5.479	50.781	1.00	22.89
3287	CA	GLN A 539	61.128	-7.943	51.314	1.00	17.53	3340	O	ARG A 545	50.354	-5.136	50.220	1.00	20.28
3288	C	GLN A 539	60.345	-7.077	52.312	1.00	18.11	3341	CB	ARG A 545	49.970	-6.500	52.565	1.00	32.05
3289	O	GLN A 539	59.366	-7.553	52.893	1.00	17.99	3342	CG	ARG A 545	49.843	-7.658	53.558	1.00	38.97
3290	CB	GLN A 539	62.351	-8.523	52.027	1.00	19.31	3343	CD	ARG A 545	48.545	-8.386	53.314	1.00	45.28
3291	CG	GLN A 539	62.149	-9.256	53.324	1.00	19.71	3344	NE	ARG A 545	47.466	-8.211	54.228	1.00	50.20
3292	CD	GLN A 539	63.417	-9.837	53.936	1.00	20.54	3345	CZ	ARG A 545	46.728	-7.225	54.696	1.00	52.67
3293	OE1	GLN A 539	64.431	-9.149	54.033	1.00	22.88	3346	NH1	ARG A 545	46.938	-5.972	54.297	1.00	54.30
3294	NE2	GLN A 539	63.404	-11.074	54.356	1.00	19.77	3347	NH2	ARG A 545	45.760	-7.508	55.581	1.00	52.76
3295	N	SER A 540	60.765	-5.844	52.489	1.00	18.42	3348	N	ILE A 546	52.568	-4.974	50.391	1.00	19.58
3296	CA	SER A 540	60.102	-4.916	53.403	1.00	20.34	3349	CA	ILE A 546	52.691	-4.154	49.197	1.00	18.16
3297	C	SER A 540	58.723	-4.480	52.906	1.00	20.30	3350	C	ILE A 546	53.570	-4.849	48.165	1.00	17.48
3298	O	SER A 540	57.763	-4.529	53.714	1.00	16.87	3351	O	ILE A 546	54.622	-5.411	48.473	1.00	13.86
3299	CB	SER A 540	61.125	-3.801	53.586	1.00	21.39	3352	CB	ILE A 546	53.198	-2.730	49.501	1.00	18.44
3300	OG	SER A 540	60.542	-2.651	54.113	1.00	26.78	3353	CG1	ILE A 546	52.267	-2.011	50.485	1.00	18.83
3301	N	LEU A 541	58.502	-4.242	51.613	1.00	17.30	3354	CG2	ILE A 546	53.319	-1.850	48.254	1.00	16.84
3302	CA	LEU A 541	57.127	-3.909	51.140	1.00	18.58	3355	CD1	ILE A 546	52.910	-0.740	51.046	1.00	20.08
3303	C	LEU A 541	56.231	-5.132	51.270	1.00	18.04	3356	N	GLY A 547	53.077	-4.958	46.936	1.00	16.21
3304	O	LEU A 541	55.047	-5.034	51.690	1.00	17.70	3357	CA	GLY A 547	53.802	-5.583	45.845	1.00	13.51
3305	CB	LEU A 541	57.128	-3.311	49.731	1.00	19.55	3358	C	GLY A 547	54.760	-4.619	45.151	1.00	14.12
3306	CG	LEU A 541	57.908	-2.022	49.522	1.00	20.99	3359	O	GLY A 547	54.720	-3.383	45.292	1.00	12.19
3307	CD1	LEU A 541	58.100	-1.486	48.104	1.00	20.76	3360	N	VAL A 548	55.614	-5.196	44.275	1.00	11.18
3308	CD2	LEU A 541	57.190	-0.836	50.210	1.00	21.46	3361	CA	VAL A 548	56.557	-4.349	43.534	1.00	11.75
3309	N	HIS A 542	56.739	-6.322	50.902	1.00	15.72	3362	C	VAL A 548	56.468	-4.674	42.042	1.00	12.64
3310	CA	HIS A 542	55.993	-7.545	50.990	1.00	17.12	3363	O	VAL A 548	56.761	-5.829	41.654	1.00	11.98
3311	C	HIS A 542	55.499	-7.790	52.421	1.00	20.37	3364	CB	VAL A 548	57.995	-4.621	43.998	1.00	13.59
3312	O	HIS A 542	54.326	-8.187	52.598	1.00	17.99	3365	CG1	VAL A 548	58.998	-3.860	43.135	1.00	15.29
3313	CB	HIS A 542	56.747	-8.783	50.476	1.00	17.02	3366	CG2	VAL A 548	58.278	-4.241	45.466	1.00	12.74
3314	CG	HIS A 542	56.882	-8.831	48.975	1.00	16.64	3367	N	ASN A 549	56.225	-3.678	41.208	1.00	12.65
3315	ND1	HIS A 542	57.700	-9.780	48.377	1.00	15.29	3368	CA	ASN A 549	56.184	-3.878	39.757	1.00	13.79
3316	CD2	HIS A 542	56.349	-8.154	47.933	1.00	14.04	3369	C	ASN A 549	57.405	-3.147	39.191	1.00	15.40
3317	CE1	HIS A 542	57.670	-9.669	47.055	1.00	15.74	3370	O	ASN A 549	57.639	-1.977	39.536	1.00	14.02
3318	NE2	HIS A 542	56.848	-8.690	46.754	1.00	14.08	3371	CB	ASN A 549	54.882	-3.275	39.173	1.00	14.17
3319	N	GLN A 543	56.340	-7.489	53.425	1.00	19.61	3372	CG	ASN A 549	53.592	-4.005	39.512	1.00	15.52
3320	CA	GLN A 543	55.955	-7.702	54.817	1.00	22.30	3373	OD1	ASN A 549	53.667	-5.127	40.037	1.00	15.71
3321	C	GLN A 543	54.786	-6.794	55.164	1.00	22.43	3374	ND2	ASN A 549	52.374	-3.530	39.214	1.00	11.04
3322	O	GLN A 543	54.023	-7.124	56.093	1.00	20.41	3375	N	MET A 550	58.240	-3.755	38.342	1.00	14.17
3323	CB	GLN A 543	57.132	-7.462	55.797	1.00	23.32	3376	CA	MET A 550	59.397	-3.031	37.813	1.00	14.20
3324	CG	GLN A 543	58.247	-8.469	55.718	1.00	26.39	3377	C	MET A 550	59.099	-2.392	36.448	1.00	14.75
3325	CD	GLN A 543	59.583	-8.082	56.334	1.00	29.94	3378	O	MET A 550	58.661	-3.107	35.535	1.00	12.87
3326	OE1	GLN A 543	60.499	-8.911	56.516	1.00	29.73	3379	CB	MET A 550	60.626	-3.948	37.655	1.00	13.94
3327	NE2	GLN A 543	59.764	-6.816	56.705	1.00	28.77	3380	CG	MET A 550	61.452	-4.226	38.909	1.00	15.03
3328	N	GLN A 544	54.621	-5.649	54.503	1.00	21.34	3381	SD	MET A 550	62.697	-5.561	38.695	1.00	14.47
3329	CA	GLN A 544	53.444	-4.814	54.771	1.00	24.96	3382	CE	MET A 550	63.764	-4.727	37.472	1.00	16.01
3330	C	GLN A 544	52.339	-5.016	53.751	1.00	23.83	3383	CA	ASP A 551	59.368	-1.092	36.301	1.00	13.68
3331	O	GLN A 544	51.495	-4.154	53.542	1.00	23.04	3384	N	ASP A 551	59.392	-0.396	35.011	1.00	14.18
3332	CB	GLN A 544	53.875	-3.348	54.782	1.00	29.05	3385	C	ASP A 551	60.610	-0.949	34.274	1.00	15.34
3333	CG	GLN A 544	54.974	-3.219	55.851	1.00	34.54	3386	O	ASP A 551	61.711	-0.908	34.871	1.00	16.12

3387	CB	ASP A 551	59.565	1.119	35.255	1.00	13.46	3440	OG1	THR A 557	71.497	-0.474	23.145	1.00	19.18
3388	CG	ASP A 551	59.452	1.990	34.034	1.00	14.83	3441	CG2	THR A 557	70.336	-2.357	24.042	1.00	18.93
3389	OD1	ASP A 551	59.595	1.439	32.872	1.00	16.30	3442	N	PHE A 558	71.196	1.800	25.663	1.00	16.05
3390	OD2	ASP A 551	59.255	3.209	34.103	1.00	12.40	3443	CA	PHE A 558	71.758	3.135	25.800	1.00	16.69
3391	N	VAL A 552	60.530	-1.561	33.107	1.00	15.18	3444	C	PHE A 558	72.400	3.664	24.505	1.00	18.93
3392	CA	VAL A 552	61.659	-2.143	32.393	1.00	14.43	3445	O	PHE A 558	72.414	4.873	24.249	1.00	16.69
3393	C	VAL A 552	61.698	-1.675	30.951	1.00	14.19	3446	CB	PHE A 558	72.838	3.164	26.910	1.00	16.19
3394	O	VAL A 552	60.693	-1.489	30.256	1.00	15.99	3447	CG	PHE A 558	74.193	2.575	26.568	1.00	16.60
3395	CB	VAL A 552	61.674	-3.691	32.386	1.00	14.09	3448	CD1	PHE A 558	74.357	1.190	26.467	1.00	16.91
3396	CG1	VAL A 552	62.001	-4.194	33.795	1.00	11.24	3449	CD2	PHE A 558	75.276	3.376	26.339	1.00	16.22
3397	CG2	VAL A 552	60.321	-4.237	31.901	1.00	11.60	3450	CE1	PHE A 558	75.602	0.649	26.161	1.00	19.59
3398	N	VAL A 553	62.900	-1.482	30.427	1.00	13.93	3451	CE2	PHE A 558	76.552	2.866	26.027	1.00	16.94
3399	CA	VAL A 553	63.153	-0.895	29.128	1.00	15.34	3452	CZ	PHE A 558	76.715	1.484	25.941	1.00	18.98
3400	C	VAL A 553	63.848	-1.812	28.140	1.00	18.26	3453	N	ASP A 559	72.989	2.777	23.711	1.00	19.99
3401	O	VAL A 553	64.912	-1.514	27.574	1.00	18.77	3454	CA	ASP A 559	73.645	3.165	22.465	1.00	24.77
3402	CB	VAL A 553	63.939	0.406	29.373	1.00	14.83	3455	C	ASP A 559	73.934	1.880	21.666	1.00	25.09
3403	CG1	VAL A 553	64.111	1.249	28.108	1.00	17.28	3456	O	ASP A 559	73.574	0.768	22.077	1.00	24.21
3404	CG2	VAL A 553	63.326	1.232	30.565	1.00	16.73	3457	CB	ASP A 559	74.907	3.979	22.708	1.00	26.93
3405	N	TYR A 554	63.251	-2.945	27.782	1.00	19.23	3458	CG	ASP A 559	75.484	4.649	21.466	1.00	31.80
3406	CA	TYR A 554	63.787	-3.864	26.789	1.00	17.41	3459	OD1	ASP A 559	76.588	5.194	21.658	1.00	31.12
3407	C	TYR A 554	63.647	-3.343	25.367	1.00	17.63	3460	OD2	ASP A 559	74.883	4.689	20.357	1.00	31.41
3408	O	TYR A 554	64.113	-4.065	24.465	1.00	18.06	3461	N	VAL A 560	74.422	2.051	20.464	1.00	24.82
3409	CB	TYR A 554	63.080	-5.237	26.873	1.00	17.61	3462	CA	VAL A 560	74.699	0.919	19.578	1.00	26.37
3410	CG1	TYR A 554	63.378	-5.873	28.232	1.00	16.57	3463	C	VAL A 560	76.162	0.933	19.226	1.00	26.33
3411	CD1	TYR A 554	64.653	-6.384	28.473	1.00	17.67	3464	O	VAL A 560	76.831	1.966	19.532	1.00	27.51
3412	CD2	TYR A 554	62.423	-5.941	29.222	1.00	16.40	3465	CB	VAL A 560	74.048	1.006	18.185	1.00	29.28
3413	CE1	TYR A 554	64.985	-6.939	29.706	1.00	17.79	3466	CG1	VAL A 560	72.537	0.936	18.394	1.00	31.23
3414	CE2	TYR A 554	62.717	-6.544	30.457	1.00	17.52	3467	CG2	VAL A 560	74.398	2.316	17.505	1.00	28.43
3415	CZ	TYR A 554	64.006	-7.002	30.692	1.00	17.50	3468	N	MET A 561	76.781	-0.011	18.554	1.00	26.30
3416	OH	TYR A 554	64.325	-7.558	31.907	1.00	17.80	3469	CA	MET A 561	78.188	-0.013	18.178	1.00	26.74
3417	N	ASN A 555	62.967	-2.210	25.106	1.00	16.07	3470	C	MET A 561	79.185	-0.198	19.320	1.00	26.30
3418	CA	ASN A 555	62.791	-1.817	23.708	1.00	15.21	3471	O	MET A 561	80.037	-1.085	19.319	1.00	24.56
3419	C	ASN A 555	64.017	-1.220	23.038	1.00	15.49	3472	CB	MET A 561	78.547	1.207	17.296	1.00	30.44
3420	O	ASN A 555	63.978	-1.070	21.805	1.00	16.91	3473	CG	MET A 561	77.954	0.954	15.881	1.00	34.34
3421	CB	ASN A 555	61.570	-0.878	23.597	1.00	15.73	3474	SD	MET A 561	78.414	2.299	14.735	1.00	41.54
3422	CG	ASN A 555	61.821	0.417	24.328	1.00	16.71	3475	CE	MET A 561	77.950	3.727	15.746	1.00	37.55
3423	OD1	ASN A 555	62.555	1.260	23.818	1.00	16.20	3476	N	VAL A 562	79.105	0.597	20.392	1.00	24.81
3424	ND2	ASN A 555	61.191	0.631	25.511	1.00	15.91	3477	CA	VAL A 562	79.878	0.473	21.588	1.00	24.01
3425	N	HIS A 556	65.054	-0.811	23.760	1.00	16.72	3478	C	VAL A 562	79.185	-0.465	22.587	1.00	22.04
3426	CA	HIS A 556	66.255	-0.226	23.128	1.00	18.73	3479	O	VAL A 562	79.767	-0.601	23.647	1.00	22.34
3427	C	HIS A 556	67.450	-0.203	24.091	1.00	18.92	3480	CB	VAL A 562	80.058	1.821	22.350	1.00	24.42
3428	O	HIS A 556	67.155	-0.343	25.279	1.00	20.30	3481	CG1	VAL A 562	80.934	2.745	21.496	1.00	24.85
3429	CB	HIS A 556	65.917	1.214	22.682	1.00	17.52	3482	CG2	VAL A 562	78.780	2.479	22.759	1.00	21.36
3430	CG	HIS A 556	65.912	2.220	23.794	1.00	18.40	3483	N	SER A 563	78.011	-1.007	22.251	1.00	20.50
3431	ND1	HIS A 556	64.764	2.524	24.490	1.00	17.65	3484	CA	SER A 563	77.297	-1.820	23.238	1.00	20.03
3432	CD2	HIS A 556	66.886	2.964	24.365	1.00	18.54	3485	C	SER A 563	77.836	-3.239	23.199	1.00	17.42
3433	CE1	HIS A 556	65.040	3.431	25.419	1.00	17.28	3486	O	SER A 563	78.348	-3.629	22.143	1.00	17.90
3434	NE2	HIS A 556	66.303	3.717	25.383	1.00	17.13	3487	CB	SER A 563	75.773	-1.854	23.035	1.00	20.21
3435	N	THR A 557	68.719	-0.043	23.692	1.00	18.38	3488	OG	SER A 563	75.504	-2.439	21.727	1.00	19.79
3436	CA	THR A 557	69.798	0.042	24.644	1.00	18.28	3489	N	ASP A 564	77.647	-3.985	24.276	1.00	15.82
3437	C	THR A 557	70.323	1.476	24.705	1.00	17.57	3490	CA	ASP A 564	78.065	-5.390	24.327	1.00	15.51
3438	O	THR A 557	69.911	2.301	23.856	1.00	14.70	3491	C	ASP A 564	77.410	-6.216	23.241	1.00	16.59
3439	CB	THR A 557	70.926	-0.963	24.352	1.00	19.68	3492	O	ASP A 564	78.055	-7.027	22.529	1.00	15.21



3493	CB	ASP A 564	77.720	-5.977	25.726	1.00	16.55	3546	CD	PRO A 570	78.844	-8.878	15.311	1.00	15.81
3494	CG	ASP A 564	78.581	-5.296	26.800	1.00	18.34	3547	N	GLN A 571	75.257	-5.746	14.775	1.00	14.50
3495	OD1	ASP A 564	79.821	-5.219	26.651	1.00	17.26	3548	CA	GLN A 571	73.918	-5.303	14.447	1.00	14.80
3496	OD2	ASP A 564	78.037	-4.798	27.810	1.00	17.62	3549	C	GLN A 571	72.705	-6.160	14.739	1.00	16.27
3497	N	PHE A 565	76.111	-5.973	23.019	1.00	13.96	3550	O	GLN A 571	71.549	-5.639	14.722	1.00	13.56
3498	CA	PHE A 565	75.399	-6.655	21.943	1.00	15.67	3551	CB	GLN A 571	73.748	-4.892	12.953	1.00	15.26
3499	C	PHE A 565	76.139	-6.483	20.593	1.00	14.63	3552	CG	GLN A 571	74.766	-3.823	12.497	1.00	15.43
3500	O	PHE A 565	76.355	-7.509	19.924	1.00	13.99	3553	CD	GLN A 571	74.503	-3.354	11.059	1.00	19.19
3501	CB	PHE A 565	73.912	-6.291	21.789	1.00	16.58	3554	OE1	GLN A 571	73.563	-3.777	10.588	1.00	18.40
3502	CG	PHE A 565	72.997	-6.694	22.894	1.00	20.85	3555	NE2	GLN A 571	75.367	-2.510	10.508	1.00	16.57
3503	CD1	PHE A 565	72.139	-5.782	23.477	1.00	26.06	3556	N	TYR A 572	72.855	-7.469	14.886	1.00	16.66
3504	CD2	PHE A 565	72.967	-7.987	23.380	1.00	23.43	3557	CA	TYR A 572	71.762	-8.426	14.967	1.00	16.46
3505	CE1	PHE A 565	71.283	-6.128	24.537	1.00	28.11	3558	C	TYR A 572	70.762	-8.214	16.097	1.00	15.79
3506	CE2	PHE A 565	72.117	-8.352	24.417	1.00	24.43	3559	O	TYR A 572	69.571	-8.534	15.888	1.00	15.97
3507	CZ	PHE A 565	71.293	-7.438	25.000	1.00	25.83	3560	CB	TYR A 572	72.356	-9.851	15.074	1.00	15.56
3508	N	ASP A 566	76.440	-5.285	20.148	1.00	14.36	3561	CG	TYR A 572	71.265	-10.918	14.864	1.00	16.45
3509	CA	ASP A 566	77.110	-5.056	18.855	1.00	15.72	3562	CD1	TYR A 572	70.668	-11.104	13.618	1.00	15.36
3510	C	ASP A 566	78.563	-5.512	18.779	1.00	17.43	3563	CD2	TYR A 572	70.776	-11.624	15.938	1.00	15.32
3511	O	ASP A 566	79.047	-5.871	17.691	1.00	19.46	3564	CE1	TYR A 572	69.678	-12.067	13.462	1.00	16.37
3512	CB	ASP A 566	77.041	-3.554	18.495	1.00	15.76	3565	CE2	TYR A 572	69.793	-12.590	15.799	1.00	16.69
3513	CG	ASP A 566	75.837	-3.207	17.621	1.00	18.28	3566	CZ	TYR A 572	69.237	-12.809	14.543	1.00	16.67
3514	OD1	ASP A 566	75.121	-4.134	17.172	1.00	17.60	3567	OH	TYR A 572	68.200	-13.718	14.410	1.00	15.39
3515	OD2	ASP A 566	75.529	-1.986	17.464	1.00	18.93	3568	N	TYR A 573	71.134	-7.671	17.246	1.00	16.43
3516	N	LYS A 567	79.280	-5.618	19.905	1.00	16.44	3569	CA	TYR A 573	70.136	-7.459	18.322	1.00	17.97
3517	CA	LYS A 567	80.648	-6.126	19.938	1.00	17.53	3570	C	TYR A 573	69.259	-6.225	18.096	1.00	17.17
3518	C	LYS A 567	80.694	-7.648	19.878	1.00	17.64	3571	O	TYR A 573	68.347	-5.946	18.884	1.00	13.58
3519	O	LYS A 567	81.712	-8.259	19.540	1.00	17.11	3572	CB	TYR A 573	70.852	-7.342	19.679	1.00	18.07
3520	CB	LYS A 567	81.414	-5.609	21.194	1.00	17.62	3573	CG	TYR A 573	71.414	-8.647	20.227	1.00	20.16
3521	CG	LYS A 567	81.622	-4.074	21.089	1.00	18.85	3574	CD1	TYR A 573	72.722	-9.044	20.012	1.00	19.58
3522	CD	LYS A 567	82.538	-3.543	22.204	1.00	18.13	3575	CD2	TYR A 573	70.603	-9.487	21.008	1.00	20.25
3523	CE	LYS A 567	81.848	-3.502	23.564	1.00	18.33	3576	CE1	TYR A 573	73.204	-10.247	20.549	1.00	20.41
3524	NZ	LYS A 567	82.816	-3.195	24.678	1.00	16.66	3577	CE2	TYR A 573	71.064	-10.682	21.552	1.00	19.87
3525	N	LIE A 568	79.612	-8.349	20.201	1.00	16.25	3578	CZ	TYR A 573	72.388	-11.041	21.317	1.00	20.91
3526	CA	LIE A 568	79.549	-9.800	20.123	1.00	16.20	3579	OH	TYR A 573	72.862	-12.222	21.864	1.00	20.44
3527	C	LIE A 568	78.908	-10.273	18.823	1.00	17.07	3580	N	TYR A 574	69.515	-5.474	17.014	1.00	16.82
3528	O	LIE A 568	79.382	-11.238	18.178	1.00	14.48	3581	CA	TYR A 574	68.727	-4.275	16.718	1.00	15.66
3529	CB	LIE A 568	78.818	-10.362	21.376	1.00	16.15	3582	C	TYR A 574	68.004	-4.350	15.382	1.00	16.73
3530	CG1	LIE A 568	79.514	-9.915	22.665	1.00	15.42	3583	O	TYR A 574	68.406	-5.134	14.504	1.00	18.00
3531	CG2	LIE A 568	78.774	-11.890	21.304	1.00	14.58	3584	CB	TYR A 574	69.665	-3.067	16.759	1.00	15.38
3532	CD1	LIE A 568	78.696	-10.199	23.951	1.00	17.78	3585	CG	TYR A 574	70.493	-2.931	18.020	1.00	18.02
3533	N	VAL A 569	77.730	-9.732	18.434	1.00	15.69	3586	CD1	TYR A 574	69.924	-2.327	19.156	1.00	17.70
3534	CA	VAL A 569	77.048	-10.133	17.196	1.00	15.88	3587	CD2	TYR A 574	71.787	-3.466	18.124	1.00	18.97
3535	C	VAL A 569	76.626	-8.839	16.471	1.00	16.98	3588	CE1	TYR A 574	70.640	-2.205	20.327	1.00	16.27
3536	O	VAL A 569	75.525	-8.306	16.695	1.00	15.04	3589	CE2	TYR A 574	72.507	-3.336	19.319	1.00	18.59
3537	CB	VAL A 569	75.807	-11.021	17.396	1.00	15.85	3590	CZ	TYR A 574	71.932	-2.685	20.399	1.00	18.97
3538	CG1	VAL A 569	75.416	-11.682	16.074	1.00	14.38	3591	OH	TYR A 574	72.633	-2.523	21.588	1.00	18.86
3539	CG2	VAL A 569	75.972	-12.073	18.504	1.00	14.02	3592	N	ARG A 575	66.949	-3.552	15.167	1.00	14.99
3540	N	PRO A 570	77.515	-8.315	15.624	1.00	15.25	3593	CA	ARG A 575	66.271	-3.493	13.869	1.00	15.92
3541	CA	PRO A 570	77.309	-7.021	14.982	1.00	16.13	3594	C	ARG A 575	66.986	-2.557	12.896	1.00	16.49
3542	C	PRO A 570	75.950	-6.794	14.359	1.00	16.17	3595	O	ARG A 575	67.443	-1.428	13.268	1.00	14.85
3543	O	PRO A 570	75.466	-7.600	13.555	1.00	15.22	3596	CB	ARG A 575	64.798	-3.050	14.073	1.00	15.06
3544	CB	PRO A 570	78.472	-6.901	14.010	1.00	17.25	3597	CG	ARG A 575	63.996	-3.916	15.070	1.00	15.86
3545	CG	PRO A 570	79.570	-7.724	14.640	1.00	16.61	3598	CD	ARG A 575	62.468	-3.788	14.882	1.00	16.88

3599	NE	ARG A 575	61.750	-4.691	15.785	1.00	13.65	3652	CE1 TYR A 582	73.853	0.831	13.960	1.00	28.48
3600	CZ	ARG A 575	61.087	-4.506	16.914	1.00	16.15	3653	CE2 TYR A 582	72.561	-0.924	15.000	1.00	28.99
3601	NH1	ARG A 575	60.840	-3.302	17.495	1.00	13.01	3654	CZ TYR A 582	73.774	-0.390	14.589	1.00	28.99
3602	NH2	ARG A 575	60.591	-5.606	17.516	1.00	11.72	3655	OH TYR A 582	74.899	-1.115	14.864	1.00	28.24
3603	N	THR A 576	67.240	-3.018	11.669	1.00	17.48	3656	N THR A 583	66.912	1.437	12.737	1.00	18.57
3604	CA	THR A 576	67.911	-2.206	10.648	1.00	16.92	3657	CA THR A 583	65.623	2.143	12.764	1.00	19.17
3605	C	THR A 576	67.062	-2.149	9.365	1.00	18.54	3658	C THR A 583	65.399	2.672	14.204	1.00	19.21
3606	O	THR A 576	66.283	-3.087	9.134	1.00	19.15	3659	O THR A 583	66.002	2.240	15.227	1.00	15.73
3607	CB	THR A 576	69.304	-2.708	10.228	1.00	17.51	3660	CB THR A 583	64.442	1.271	12.295	1.00	21.01
3608	OG1	THR A 576	69.224	-4.053	9.768	1.00	12.75	3661	OG1 THR A 583	64.334	0.091	13.179	1.00	19.15
3609	CG2	THR A 576	70.351	-2.561	11.345	1.00	18.13	3662	CG2 THR A 583	64.598	0.758	10.847	1.00	20.19
3610	N	ASP A 577	67.206	-1.088	8.567	1.00	18.10	3663	N ASN A 584	64.574	3.728	14.303	1.00	16.30
3611	CA	ASP A 577	66.406	-0.999	7.351	1.00	18.80	3664	CA ASN A 584	64.420	4.507	15.514	1.00	17.48
3612	C	ASP A 577	67.218	-1.512	6.154	1.00	20.47	3665	C ASN A 584	63.063	4.434	16.164	1.00	17.05
3613	O	ASP A 577	68.348	-2.037	6.306	1.00	22.66	3666	O ASN A 584	62.469	5.447	16.559	1.00	16.19
3614	CB	ASP A 577	65.858	0.404	7.051	1.00	18.16	3667	CB ASN A 584	64.779	5.966	15.133	1.00	19.28
3615	CG	ASP A 577	66.941	1.424	6.856	1.00	19.10	3668	CG ASN A 584	65.141	6.823	16.319	1.00	20.58
3616	OD1	ASP A 577	66.636	2.634	7.169	1.00	19.08	3669	OD1 ASN A 584	65.304	6.339	17.435	1.00	22.86
3617	OD2	ASP A 577	68.119	1.198	6.485	1.00	16.70	3670	ND2 ASN A 584	65.101	8.148	16.199	1.00	22.27
3618	N	SER A 578	66.674	-1.364	4.963	1.00	20.77	3671	N GLY A 585	62.499	3.249	16.338	1.00	17.36
3619	CA	SER A 578	67.276	-1.837	3.705	1.00	21.43	3672	CA GLY A 585	61.169	3.095	16.940	1.00	18.20
3620	C	SER A 578	68.503	-1.061	3.308	1.00	21.24	3673	C GLY A 585	61.073	3.688	18.348	1.00	19.43
3621	O	SER A 578	69.334	-1.575	2.544	1.00	21.58	3674	O GLY A 585	60.000	4.151	18.739	1.00	17.42
3622	CB	SER A 578	66.212	-1.815	2.599	1.00	23.81	3675	N SER A 586	62.149	3.685	19.128	1.00	20.93
3623	OG	SER A 578	65.419	-2.993	2.665	1.00	24.09	3676	CA SER A 586	62.095	4.195	20.490	1.00	21.54
3624	N	ASN A 579	68.692	0.150	3.800	1.00	21.04	3677	C SER A 586	62.259	5.711	20.590	1.00	20.81
3625	CA	ASN A 579	69.893	0.918	3.551	1.00	22.84	3678	O SER A 586	61.993	6.277	21.652	1.00	20.13
3626	C	ASN A 579	71.069	0.581	4.470	1.00	22.28	3679	CB SER A 586	63.221	3.538	21.302	1.00	20.63
3627	O	ASN A 579	72.244	1.070	4.370	1.00	22.77	3680	OG SER A 586	64.491	4.039	20.840	1.00	21.23
3628	CB	ASN A 579	69.572	2.403	3.670	1.00	24.77	3681	N GLY A 587	63.102	7.781	19.629	1.00	21.87
3629	CG	ASN A 579	68.611	2.929	2.641	1.00	27.96	3682	C GLY A 587	64.469	8.006	20.279	1.00	21.87
3630	OD1	ASN A 579	67.940	3.947	2.900	1.00	30.34	3683	CA GLY A 587	64.930	9.158	20.346	1.00	21.43
3631	ND2	ASN A 579	68.431	2.198	1.548	1.00	27.67	3684	O GLY A 587	65.213	6.945	20.630	1.00	19.06
3632	N	GLY A 580	70.811	-0.191	5.501	1.00	21.69	3685	N CYS A 588	66.495	7.043	21.300	1.00	19.09
3633	CA	GLY A 580	71.749	-0.563	6.551	1.00	20.67	3686	CA CYS A 588	67.651	6.569	20.417	1.00	20.16
3634	C	GLY A 580	71.708	0.335	7.781	1.00	20.28	3687	O CYS A 588	68.797	6.442	20.864	1.00	18.88
3635	O	GLY A 580	72.723	0.373	8.505	1.00	20.34	3688	C CYS A 588	66.462	6.167	22.569	1.00	18.06
3636	N	ASN A 581	70.727	1.230	7.907	1.00	19.77	3689	CB CYS A 588	65.249	6.772	23.792	1.00	20.94
3637	CA	ASN A 581	70.647	2.096	9.057	1.00	20.14	3690	SG CYS A 588	67.358	6.343	19.130	1.00	19.74
3638	C	ASN A 581	69.811	1.448	10.186	1.00	20.05	3691	N GLY A 589	68.464	5.999	18.224	1.00	20.77
3639	O	ASN A 581	68.809	0.802	9.843	1.00	20.06	3692	CA GLY A 589	68.511	4.521	17.843	1.00	20.75
3640	CB	ASN A 581	70.061	3.486	8.758	1.00	20.77	3693	C GLY A 589	68.511	4.521	17.843	1.00	20.75
3641	CG	ASN A 581	70.979	4.271	7.815	1.00	24.55	3694	O GLY A 589	69.319	4.222	16.957	1.00	21.38
3642	OD1	ASN A 581	72.201	4.336	7.991	1.00	25.71	3695	N ASN A 590	67.768	3.611	18.454	1.00	18.78
3643	ND2	ASN A 581	70.436	4.847	6.760	1.00	22.88	3696	CA ASN A 590	67.823	2.183	18.077	1.00	17.60
3644	N	TYR A 582	70.211	1.744	11.428	1.00	18.90	3697	C ASN A 590	66.576	1.529	18.652	1.00	17.96
3645	CA	TYR A 582	69.377	1.345	12.592	1.00	20.45	3698	O ASN A 590	65.865	2.190	19.463	1.00	17.56
3646	C	TYR A 582	68.045	2.071	12.591	1.00	18.67	3699	CB ASN A 590	69.087	1.484	18.624	1.00	15.88
3647	O	TYR A 582	68.050	3.319	12.396	1.00	17.45	3700	CG ASN A 590	69.144	1.355	20.139	1.00	17.35
3648	CB	TYR A 582	70.093	1.730	13.900	1.00	21.60	3701	OD1 ASN A 590	68.469	0.536	20.774	1.00	15.30
3649	CG	TYR A 582	71.394	0.997	14.143	1.00	26.25	3702	ND2 ASN A 590	69.897	2.207	20.808	1.00	15.71
3650	CD1	TYR A 582	72.639	1.501	13.726	1.00	27.97	3703	N GLU A 591	66.335	0.275	18.302	1.00	17.77
3651	CD2	TYR A 582	71.374	-0.230	14.777	1.00	27.31	3704	CA GLU A 591	65.200	-0.435	18.873	1.00	18.01

3705	C	GLU A 591	65.575	-1.923	18.828	1.00	18.01	3758	CB	PRO A 597	64.928	-16.799	17.319	1.00	17.50
3706	O	GLU A 591	66.264	-2.419	17.909	1.00	17.69	3759	CG	PRO A 597	64.306	-16.514	15.953	1.00	18.51
3707	CB	GLU A 591	68.831	-0.072	18.251	1.00	19.26	3760	CD	PRO A 598	64.817	-15.129	15.637	1.00	18.53
3708	CG	GLU A 591	63.658	-0.382	16.805	1.00	18.33	3761	N	MET A 598	66.964	-15.173	19.087	1.00	15.98
3709	CD	GLU A 591	62.322	-0.090	16.134	1.00	19.76	3762	CA	MET A 598	67.874	-15.133	20.231	1.00	15.82
3710	OE1	GLU A 591	62.383	0.617	15.092	1.00	18.91	3763	C	MET A 598	67.729	-13.791	20.940	1.00	15.34
3711	OE2	GLU A 591	61.249	0.589	16.551	1.00	18.36	3764	O	MET A 598	68.082	-13.708	22.130	1.00	16.95
3712	N	PHE A 592	65.262	-2.635	19.900	1.00	15.35	3765	CB	MET A 598	69.336	-15.412	19.803	1.00	16.00
3713	CA	PHE A 592	65.646	-4.041	20.070	1.00	18.51	3766	CG	MET A 598	69.574	-16.841	19.325	1.00	13.68
3714	C	PHE A 592	64.787	-4.958	19.219	1.00	16.58	3767	SD	MET A 598	69.207	-18.085	20.579	1.00	13.98
3715	O	PHE A 592	63.532	-4.916	19.203	1.00	18.31	3768	CE	MET A 598	70.593	-17.828	21.697	1.00	15.11
3716	CB	PHE A 592	65.507	-4.330	21.572	1.00	18.66	3769	N	ALA A 599	67.344	-12.740	20.202	1.00	14.72
3717	CG	PHE A 592	66.320	-5.575	22.007	1.00	19.55	3770	CA	ALA A 599	67.059	-11.481	20.876	1.00	15.20
3718	CD1	PHE A 592	67.687	-5.484	22.227	1.00	21.67	3771	C	ALA A 599	65.749	-11.281	22.874	1.00	16.47
3719	CD2	PHE A 592	65.700	-6.800	22.204	1.00	21.14	3772	O	ALA A 599	65.783	-11.665	21.708	1.00	17.10
3720	CE1	PHE A 592	68.400	-6.593	22.666	1.00	21.13	3773	CB	ALA A 599	66.943	-10.328	19.898	1.00	13.55
3721	CE2	PHE A 592	66.399	-7.894	22.657	1.00	21.68	3774	N	GLN A 600	64.731	-12.308	21.178	1.00	16.72
3722	CZ	PHE A 592	67.750	-7.786	22.877	1.00	20.22	3775	CA	GLN A 600	63.525	-12.575	21.946	1.00	18.51
3723	N	ALA A 593	65.422	-5.805	18.433	1.00	15.23	3776	C	GLN A 600	63.860	-13.406	23.201	1.00	17.76
3724	CA	ALA A 593	64.731	-6.643	17.459	1.00	14.58	3777	O	GLN A 600	63.429	-13.048	24.311	1.00	13.69
3725	C	ALA A 593	64.218	-7.941	18.052	1.00	15.78	3778	CB	GLN A 600	62.404	-13.240	21.137	1.00	17.71
3726	O	ALA A 593	64.818	-8.986	17.839	1.00	15.37	3779	CG	GLN A 600	61.117	-13.534	21.935	1.00	16.56
3727	CB	ALA A 593	65.653	-6.921	16.263	1.00	14.49	3780	CD	GLN A 600	60.174	-14.357	21.052	1.00	16.99
3728	N	THR A 594	63.084	-7.909	18.737	1.00	13.64	3781	OE1	GLN A 600	60.365	-15.573	20.886	1.00	17.99
3729	CA	THR A 594	62.430	-9.049	19.319	1.00	17.21	3782	NE2	GLN A 600	59.183	-13.690	20.475	1.00	12.76
3730	C	THR A 594	61.878	-10.007	18.255	1.00	18.41	3783	N	LYS A 601	64.723	-14.418	23.042	1.00	17.63
3731	O	THR A 594	61.673	-11.162	18.635	1.00	16.76	3784	CA	LYS A 601	65.138	-15.279	24.130	1.00	17.70
3732	CB	THR A 594	61.234	-8.677	20.250	1.00	15.31	3785	C	LYS A 601	65.881	-14.783	26.399	1.00	16.32
3733	CG1	THR A 594	60.306	-7.885	19.481	1.00	16.09	3786	O	LYS A 601	65.662	-14.783	26.399	1.00	18.32
3734	CG2	THR A 594	61.715	-7.890	21.453	1.00	15.49	3787	CB	LYS A 601	66.023	-16.457	23.633	1.00	18.32
3735	N	GLU A 595	61.866	-9.680	16.956	1.00	17.58	3788	CG	LYS A 601	66.619	-17.286	24.778	1.00	17.88
3736	CA	GLU A 595	61.519	-10.670	15.952	1.00	17.42	3789	CD	LYS A 601	67.393	-18.512	24.279	1.00	18.60
3737	C	GLU A 595	62.715	-11.589	15.648	1.00	18.14	3790	CE	LYS A 601	68.237	-19.167	25.397	1.00	18.85
3738	O	GLU A 595	62.627	-12.532	14.859	1.00	19.18	3791	NZ	LYS A 601	67.398	-19.618	26.571	1.00	16.70
3739	CB	GLU A 595	60.966	-10.097	14.646	1.00	18.92	3792	N	PHE A 602	66.732	-13.517	24.854	1.00	17.63
3740	CG	GLU A 595	61.955	-9.284	13.797	1.00	17.41	3793	CA	PHE A 602	67.370	-12.649	25.854	1.00	16.13
3741	CD	GLU A 595	62.127	-7.889	14.333	1.00	18.02	3794	C	PHE A 602	66.329	-12.012	26.764	1.00	16.27
3742	OE1	GLU A 595	61.964	-7.461	15.493	1.00	16.28	3795	O	PHE A 602	66.554	-11.907	28.009	1.00	14.81
3743	OE2	GLU A 595	62.768	-7.075	13.557	1.00	18.81	3796	C	PHE A 602	68.204	-11.538	25.161	1.00	16.06
3744	N	HIS A 596	63.900	-11.351	16.189	1.00	16.45	3797	CB	PHE A 602	68.846	-10.590	26.149	1.00	16.65
3745	CA	HIS A 596	65.050	-12.239	15.996	1.00	15.59	3798	CD1	PHE A 602	70.050	-10.983	26.751	1.00	15.22
3746	C	HIS A 596	65.076	-13.182	17.190	1.00	16.08	3799	CD2	PHE A 602	68.204	-11.538	26.149	1.00	17.45
3747	O	HIS A 596	65.031	-12.701	18.324	1.00	14.25	3800	CE1	PHE A 602	70.620	-10.201	27.747	1.00	17.98
3748	CB	HIS A 596	66.324	-11.404	15.934	1.00	15.72	3801	CE2	PHE A 602	70.006	-9.011	28.135	1.00	15.11
3749	CG	HIS A 596	66.598	-10.769	14.592	1.00	16.18	3802	CZ	PHE A 602	65.258	-11.426	26.171	1.00	15.45
3750	ND1	HIS A 596	67.579	-9.788	14.434	1.00	14.53	3803	N	VAL A 603	64.237	-10.777	27.017	1.00	15.99
3751	CD1	HIS A 596	66.014	-10.918	13.388	1.00	13.81	3804	CA	VAL A 603	64.237	-11.778	27.884	1.00	16.06
3752	CE1	HIS A 596	67.617	-9.420	13.163	1.00	15.09	3805	C	VAL A 603	63.494	-11.778	27.884	1.00	16.06
3753	NE2	HIS A 596	66.708	-10.116	12.524	1.00	15.29	3806	O	VAL A 603	63.312	-11.545	29.095	1.00	16.02
3754	N	PRO A 597	64.965	-14.485	16.976	1.00	16.49	3807	CB	VAL A 603	63.212	-9.946	26.186	1.00	18.42
3755	CA	PRO A 597	64.763	-15.436	18.023	1.00	17.55	3808	CG1	VAL A 603	62.219	-9.197	27.073	1.00	14.68
3756	C	PRO A 597	65.654	-15.307	19.250	1.00	18.38	3809	CG2	VAL A 603	63.961	-8.957	25.276	1.00	15.72
3757	O	PRO A 597	65.097	-15.446	20.358	1.00	17.58	3810	N	LEU A 604	63.039	-12.897	27.353	1.00	13.96

3811	CA	LEU A 604	62.322	-13.923	28.086	1.00	15.23	3864	CG	TRP A 610	64.795	-8.841	36.758	1.00	17.32
3812	C	LEU A 604	63.112	-14.470	29.269	1.00	17.26	3865	CD1	TRP A 610	65.385	-8.826	35.530	1.00	18.14
3813	O	LEU A 604	62.593	-14.609	30.374	1.00	14.68	3866	CD2	TRP A 610	65.604	-8.000	37.606	1.00	16.87
3814	CB	LEU A 604	61.903	-15.076	27.150	1.00	18.02	3867	NE1	TRP A 610	66.501	-8.032	35.528	1.00	17.52
3815	CG	LEU A 604	60.794	-14.774	26.119	1.00	19.15	3868	CE2	TRP A 610	66.670	-7.524	36.816	1.00	17.86
3816	CD1	LEU A 604	60.645	-15.892	25.085	1.00	19.70	3869	CE3	TRP A 610	65.507	-7.619	38.949	1.00	16.40
3817	CD2	LEU A 604	59.464	-14.593	26.844	1.00	21.10	3870	CZ2	TRP A 610	67.624	-6.629	37.310	1.00	17.05
3818	N	ASP A 605	64.415	-14.727	29.072	1.00	15.26	3871	CC3	TRP A 610	66.480	-6.768	39.473	1.00	18.04
3819	CA	ASP A 605	65.315	-15.216	30.095	1.00	16.47	3872	CH2	TRP A 610	67.519	-6.256	38.646	1.00	16.76
3820	C	ASP A 605	65.424	-14.164	31.216	1.00	16.78	3873	N	VAL A 611	61.917	-12.259	38.217	1.00	17.68
3821	O	ASP A 605	65.426	-14.517	32.390	1.00	15.91	3874	CA	VAL A 611	60.891	-12.872	39.051	1.00	17.19
3822	CB	ASP A 605	66.722	-15.477	29.523	1.00	14.57	3875	C	VAL A 611	61.481	-13.944	39.976	1.00	17.50
3823	CG	ASP A 605	66.881	-16.749	28.698	1.00	18.15	3876	O	VAL A 611	61.150	-13.951	41.159	1.00	17.52
3824	OD1	ASP A 605	67.938	-16.953	28.012	1.00	14.80	3877	CB	VAL A 611	59.784	-13.473	38.166	1.00	16.45
3825	OD2	ASP A 605	65.927	-17.564	28.720	1.00	15.40	3878	CG1	VAL A 611	58.825	-14.397	38.941	1.00	13.42
3826	N	SER A 606	65.555	-12.903	30.809	1.00	15.59	3879	CG2	VAL A 611	58.959	-12.335	37.537	1.00	15.16
3827	CA	SER A 606	65.716	-11.772	31.721	1.00	14.83	3880	N	ASN A 612	62.221	-14.917	39.491	1.00	17.95
3828	C	SER A 606	64.501	-11.560	32.614	1.00	14.39	3881	CA	ASN A 612	62.770	-15.986	40.314	1.00	19.97
3829	O	SER A 606	64.675	-11.460	33.840	1.00	13.45	3882	C	ASN A 612	63.769	-15.479	41.361	1.00	20.64
3830	CB	SER A 606	66.094	-10.483	30.977	1.00	14.58	3883	O	ASN A 612	63.629	-15.773	42.566	1.00	20.67
3831	OG	SER A 606	66.281	-9.390	31.898	1.00	14.28	3884	CB	ASN A 612	63.350	-17.062	39.398	1.00	23.07
3832	N	VAL A 607	63.265	-11.480	32.095	1.00	14.64	3885	CG	ASN A 612	62.330	-17.925	38.661	1.00	27.67
3833	CA	VAL A 607	62.127	-11.281	33.004	1.00	15.38	3886	OD1	ASN A 612	62.706	-18.413	37.561	1.00	30.76
3834	C	VAL A 607	61.945	-12.521	33.896	1.00	15.96	3887	ND2	ASN A 612	61.091	-18.211	39.114	1.00	23.39
3835	O	VAL A 607	61.514	-12.318	35.035	1.00	15.28	3888	N	GLU A 613	64.994	-14.722	40.987	1.00	17.75
3836	CB	VAL A 607	60.810	-10.937	32.280	1.00	15.47	3889	CA	GLU A 613	65.784	-14.237	41.933	1.00	16.91
3837	CG1	VAL A 607	60.974	-9.551	31.618	1.00	13.87	3890	C	GLU A 613	65.325	-13.120	42.851	1.00	16.20
3838	CG2	VAL A 607	60.425	-12.035	31.264	1.00	12.85	3891	O	GLU A 613	65.810	-13.011	44.017	1.00	15.78
3839	N	ASN A 608	62.193	-13.746	33.446	1.00	14.92	3892	CB	GLU A 613	67.044	-13.805	41.121	1.00	17.72
3840	CA	ASN A 608	62.161	-14.916	34.299	1.00	16.74	3893	CG	GLU A 613	68.292	-13.483	41.942	1.00	17.78
3841	C	ASN A 608	63.201	-14.835	35.444	1.00	17.85	3894	CD	GLU A 613	68.895	-14.683	42.660	1.00	19.51
3842	O	ASN A 608	62.877	-15.128	36.608	1.00	17.58	3895	OE1	GLU A 613	68.818	-15.820	42.180	1.00	18.15
3843	CB	ASN A 608	62.493	-16.209	33.518	1.00	19.59	3896	OE2	GLU A 613	69.413	-14.521	43.782	1.00	21.38
3844	CG	ASN A 608	61.296	-16.876	32.872	1.00	22.08	3897	N	TYR A 614	64.583	-12.123	42.358	1.00	14.53
3845	OD1	ASN A 608	60.979	-16.711	31.678	1.00	25.08	3898	CA	TYR A 614	64.252	-10.958	43.180	1.00	14.18
3846	ND2	ASN A 608	60.495	-17.611	33.626	1.00	20.95	3899	C	TYR A 614	62.805	-11.002	43.696	1.00	17.41
3847	N	TYR A 609	64.415	-14.328	35.175	1.00	15.99	3900	O	TYR A 614	62.446	-10.102	44.461	1.00	17.30
3848	CA	TYR A 609	65.427	-14.137	36.228	1.00	15.94	3901	CB	TYR A 614	64.553	-9.677	42.390	1.00	13.30
3849	C	TYR A 609	64.972	-13.130	37.284	1.00	17.05	3902	CG	TYR A 614	66.058	-9.370	42.201	1.00	14.37
3850	O	TYR A 609	65.128	-13.371	38.504	1.00	15.91	3903	CD1	TYR A 614	66.759	-8.589	43.088	1.00	14.58
3851	CB	TYR A 609	66.775	-13.708	35.575	1.00	15.56	3904	CD2	TYR A 614	66.753	-9.907	41.128	1.00	13.92
3852	CG	TYR A 609	67.853	-13.313	36.573	1.00	16.22	3905	CE1	TYR A 614	68.139	-8.317	42.936	1.00	14.22
3853	CD1	TYR A 609	68.489	-14.266	37.390	1.00	16.45	3906	CE2	TYR A 614	68.120	-9.659	40.942	1.00	13.85
3854	CD2	TYR A 609	68.197	-12.002	36.736	1.00	16.36	3907	CZ	TYR A 614	68.795	-8.864	41.857	1.00	15.00
3855	CE1	TYR A 609	69.470	-13.877	38.289	1.00	17.53	3908	OH	TYR A 614	70.152	-8.611	41.699	1.00	13.86
3856	CE2	TYR A 609	69.169	-11.603	37.661	1.00	17.03	3909	N	HIS A 615	61.982	-11.968	43.309	1.00	16.00
3857	CZ	TYR A 609	69.731	-12.544	38.487	1.00	17.07	3910	CA	HIS A 615	60.589	-12.094	43.716	1.00	18.34
3858	OH	TYR A 609	70.710	-12.140	39.389	1.00	18.77	3911	C	HIS A 615	59.671	-10.919	43.363	1.00	18.85
3859	N	TRP A 610	64.391	-11.975	36.873	1.00	15.33	3912	O	HIS A 615	58.762	-10.588	44.142	1.00	19.15
3860	CA	TRP A 610	63.997	-10.954	37.843	1.00	14.87	3913	CB	HIS A 615	60.472	-12.330	45.226	1.00	19.79
3861	C	TRP A 610	62.906	-11.516	38.749	1.00	17.00	3914	CG	HIS A 615	61.244	-13.480	45.789	1.00	21.80
3862	O	TRP A 610	62.946	-11.295	39.934	1.00	15.43	3915	ND1	HIS A 615	61.349	-13.681	47.151	1.00	22.61
3863	CB	TRP A 610	63.571	-9.617	37.205	1.00	16.60	3916	CD2	HIS A 615	62.034	-14.415	45.189	1.00	23.99

3917	CE1	HIS	A	615	62.102	-14.765	47.345	1.00	24.07	3970	CZ	PHE	A	621	57.224	-7.266	30.597	1.00	15.91
3918	NE2	HIS	A	615	62.561	-15.201	46.179	1.00	24.55	3971	N	ASP	A	622	58.055	-0.182	29.255	1.00	16.73
3919	N	VAL	A	616	59.898	-10.221	42.256	1.00	18.17	3972	CA	ASP	A	622	58.232	1.100	28.539	1.00	17.39
3920	CA	VAL	A	616	59.090	-9.071	41.856	1.00	19.87	3973	C	ASP	A	622	57.977	0.876	27.031	1.00	17.25
3921	C	VAL	A	616	57.723	-9.605	41.412	1.00	18.87	3974	O	ASP	A	622	58.434	-0.189	26.565	1.00	14.93
3922	O	VAL	A	616	57.590	-10.767	41.010	1.00	16.35	3975	CB	ASP	A	622	59.739	1.393	28.604	1.00	16.80
3923	CB	VAL	A	616	59.829	-8.264	40.774	1.00	21.79	3976	CG	ASP	A	622	60.044	2.811	28.095	1.00	18.67
3924	CG1	VAL	A	616	61.242	-7.865	41.282	1.00	19.85	3977	OD1	ASP	A	622	59.447	3.734	28.583	1.00	16.60
3925	CG2	VAL	A	616	59.980	-9.080	39.511	1.00	22.01	3978	OD2	ASP	A	622	60.871	2.977	27.145	1.00	18.13
3926	N	ASP	A	617	56.694	-8.777	41.512	1.00	16.55	3979	N	LEU	A	623	57.278	1.764	26.338	1.00	14.28
3927	CA	ASP	A	617	55.309	-9.174	41.337	1.00	17.29	3980	CA	LEU	A	623	56.984	1.619	24.923	1.00	15.86
3928	C	ASP	A	617	54.694	-8.774	39.989	1.00	17.05	3981	C	LEU	A	623	56.733	0.197	24.536	1.00	15.06
3929	O	ASP	A	617	53.493	-9.039	39.778	1.00	14.04	3982	O	LEU	A	623	57.346	-0.346	23.597	1.00	16.48
3930	CB	ASP	A	617	54.484	-8.457	42.450	1.00	15.59	3983	CB	LEU	A	623	58.151	2.214	24.052	1.00	14.51
3931	CG	ASP	A	617	55.057	-8.762	43.825	1.00	18.73	3984	CG	LEU	A	623	58.401	3.692	24.416	1.00	16.34
3932	OD1	ASP	A	617	55.655	-7.918	44.531	1.00	18.45	3985	CD1	LEU	A	623	59.675	4.160	23.681	1.00	16.33
3933	OD2	ASP	A	617	54.889	-9.919	44.243	1.00	17.15	3986	CD2	LEU	A	623	59.877	4.593	24.089	1.00	13.45
3934	N	GLY	A	618	55.464	-8.049	39.176	1.00	15.87	3987	N	MET	A	624	55.835	-0.489	25.247	1.00	15.49
3935	CA	GLY	A	618	54.873	-7.628	37.888	1.00	16.30	3988	CA	MET	A	624	55.522	-1.877	25.003	1.00	13.19
3936	C	GLY	A	618	55.813	-6.711	37.149	1.00	15.86	3989	C	MET	A	624	55.102	-2.198	23.584	1.00	16.10
3937	O	PHE	A	619	56.907	-6.366	37.645	1.00	16.89	3990	O	MET	A	624	55.275	-3.346	23.112	1.00	13.77
3938	N	PHE	A	619	55.484	-6.362	35.912	1.00	15.02	3991	CB	MET	A	624	54.406	-2.290	25.999	1.00	14.22
3939	CA	PHE	A	619	56.312	-5.472	35.083	1.00	14.50	3992	CG	MET	A	624	54.070	-3.777	26.030	1.00	14.94
3940	C	PHE	A	619	55.488	-4.376	34.420	1.00	15.17	3993	SD	MET	A	624	52.877	-4.324	27.305	1.00	14.57
3941	O	PHE	A	619	54.403	-4.681	33.856	1.00	13.52	3994	CE	MET	A	624	51.421	-3.499	26.628	1.00	14.71
3942	CB	PHE	A	619	56.997	-6.325	33.956	1.00	14.48	3995	N	ALA	A	625	54.506	-1.234	22.820	1.00	15.88
3943	CG	PHE	A	619	58.073	-7.230	34.506	1.00	16.81	3996	CA	ALA	A	625	54.068	-1.599	21.477	1.00	16.48
3944	CD1	PHE	A	619	59.281	-6.690	34.973	1.00	16.56	3997	C	ALA	A	625	55.250	-2.159	20.679	1.00	16.42
3945	CD2	PHE	A	619	57.858	-8.593	34.669	1.00	16.67	3998	O	ALA	A	625	55.086	-3.090	19.890	1.00	14.03
3946	CE1	PHE	A	619	60.255	-7.484	35.545	1.00	15.02	3999	CB	ALA	A	625	53.509	-0.409	20.706	1.00	16.88
3947	CE2	PHE	A	619	58.854	-9.403	35.213	1.00	15.82	4000	N	LEU	A	626	56.430	-1.596	20.853	1.00	16.65
3948	CZ	PHE	A	619	60.044	-8.841	35.642	1.00	15.77	4001	CA	LEU	A	626	57.627	-2.049	20.152	1.00	17.27
3949	N	ARG	A	620	56.013	-3.165	34.311	1.00	13.06	4002	C	LEU	A	626	58.839	-4.029	19.551	1.00	18.64
3950	CA	ARG	A	620	55.491	-2.106	33.449	1.00	14.20	4003	O	LEU	A	626	58.766	-1.121	20.566	1.00	18.21
3951	C	ARG	A	620	56.455	-1.959	32.251	1.00	13.44	4004	CB	LEU	A	626	58.766	-1.121	20.566	1.00	17.52
3952	O	ARG	A	620	56.455	-1.959	32.251	1.00	13.44	4005	CG	LEU	A	626	58.661	0.383	20.154	1.00	17.88
3953	CB	ARG	A	620	55.343	-0.758	34.177	1.00	14.29	4006	CD1	LEU	A	626	59.903	1.092	20.758	1.00	16.85
3954	CG	ARG	A	620	55.343	-0.758	34.177	1.00	14.29	4007	CD2	LEU	A	626	58.680	0.441	18.639	1.00	17.72
3955	CD	ARG	A	620	56.325	1.383	33.136	1.00	15.20	4008	N	LEU	A	627	57.659	-4.144	21.467	1.00	16.19
3956	NE	ARG	A	620	55.937	2.660	32.513	1.00	16.32	4009	CA	LEU	A	627	58.113	-5.513	21.759	1.00	15.53
3957	CZ	ARG	A	620	56.625	3.360	31.605	1.00	17.13	4010	C	LEU	A	627	57.363	-6.526	20.913	1.00	16.98
3958	NH1	ARG	A	620	57.796	2.947	31.125	1.00	13.61	4011	O	LEU	A	627	57.855	-7.855	19.681	1.00	17.15
3959	NH2	ARG	A	620	56.155	-4.529	31.132	1.00	15.70	4012	CB	LEU	A	627	57.921	-5.793	23.258	1.00	13.38
3960	N	PHE	A	621	56.083	-2.274	31.031	1.00	14.29	4013	CG	LEU	A	627	58.686	-4.849	24.212	1.00	15.02
3961	CA	PHE	A	621	56.956	-2.250	29.884	1.00	16.71	4014	CD1	LEU	A	627	58.414	-5.232	23.681	1.00	15.03
3962	C	PHE	A	621	56.956	-0.918	29.145	1.00	17.64	4015	CD2	LEU	A	627	60.170	-4.930	23.934	1.00	14.76
3963	O	PHE	A	621	55.903	-0.563	28.593	1.00	16.47	4016	N	GLY	A	628	56.185	-6.119	20.421	1.00	17.12
3964	CB	PHE	A	621	56.636	-3.381	28.868	1.00	17.26	4017	CA	GLY	A	628	55.382	-6.956	19.534	1.00	18.12
3965	CG	PHE	A	621	56.868	-4.750	29.455	1.00	17.89	4018	C	GLY	A	628	54.439	-7.946	20.204	1.00	17.72
3966	CD1	PHE	A	621	58.079	-5.403	29.341	1.00	15.81	4019	O	GLY	A	628	54.669	-8.439	21.306	1.00	16.57
3967	CD2	PHE	A	621	55.812	-5.373	30.137	1.00	17.10	4020	N	LYS	A	629	53.318	-8.265	19.560	1.00	18.93
3968	CE1	PHE	A	621	58.263	-6.641	29.911	1.00	16.43	4021	CA	LYS	A	629	52.277	-9.137	20.075	1.00	20.91
3969	CE2	PHE	A	621	56.005	-6.626	30.688	1.00	16.26	4022	C	LYS	A	629	52.713	-10.539	20.453	1.00	19.69

4023	O	LXS A 629	52.362	-11.008	21.533	1.00	16.07
4024	CB	LXS A 629	51.156	-9.305	19.012	1.00	25.01
4025	CG	LXS A 629	49.955	-8.430	19.255	1.00	30.66
4026	CD	LXS A 629	48.648	-9.053	18.751	1.00	34.60
4027	CE	LXS A 629	48.662	-9.270	17.249	1.00	36.35
4028	NZ	LXS A 629	47.246	-9.312	16.726	1.00	39.65
4029	N	ASP A 630	53.433	-11.217	19.563	1.00	19.67
4030	CA	ASP A 630	53.949	-12.557	19.788	1.00	21.78
4031	C	ASP A 630	54.931	-12.616	20.960	1.00	18.85
4032	O	ASP A 630	54.849	-13.490	21.817	1.00	18.70
4033	CB	ASP A 630	54.660	-13.041	18.517	1.00	26.04
4034	CG	ASP A 630	53.695	-13.269	17.360	1.00	31.74
4035	OD1	ASP A 630	54.169	-13.303	16.193	1.00	34.75
4036	OD2	ASP A 630	52.469	-13.434	17.529	1.00	33.72
4037	N	THR A 631	55.845	-11.675	21.097	1.00	18.89
4038	CA	THR A 631	56.697	-11.571	22.286	1.00	17.67
4039	C	THR A 631	55.928	-11.360	23.584	1.00	17.16
4040	O	THR A 631	56.197	-12.037	24.596	1.00	17.74
4041	CB	THR A 631	57.728	-10.455	22.062	1.00	16.84
4042	CG1	THR A 631	58.509	-10.815	20.895	1.00	16.86
4043	CG2	THR A 631	58.658	-10.288	23.259	1.00	14.40
4044	N	MET A 632	54.947	-10.471	23.613	1.00	15.74
4045	CA	MET A 632	54.128	-10.195	24.787	1.00	16.10
4046	C	MET A 632	53.304	-11.399	25.193	1.00	16.17
4047	O	MET A 632	53.196	-11.659	26.389	1.00	16.17
4048	CB	MET A 632	53.256	-8.950	24.696	1.00	14.99
4049	CG	MET A 632	53.997	-7.596	24.713	1.00	13.86
4050	SD	MET A 632	55.378	-7.434	25.863	1.00	14.63
4051	CE	MET A 632	54.506	-7.782	27.400	1.00	16.56
4052	N	ALA A 633	52.764	-12.173	24.245	1.00	17.61
4053	CA	ALA A 633	52.008	-13.370	24.597	1.00	17.78
4054	C	ALA A 633	52.902	-14.414	25.286	1.00	18.00
4055	O	ALA A 633	52.463	-15.073	26.245	1.00	15.84
4056	CB	ALA A 633	51.391	-13.971	23.328	1.00	16.07
4057	N	LXS A 634	54.135	-14.550	24.791	1.00	18.45
4058	CA	LXS A 634	55.101	-15.503	25.368	1.00	19.92
4059	C	LXS A 634	55.571	-15.082	26.757	1.00	19.10
4060	O	LXS A 634	55.753	-15.910	27.661	1.00	16.95
4061	CB	LXS A 634	56.365	-15.667	24.495	1.00	21.98
4062	CG	LXS A 634	56.109	-16.327	23.139	1.00	25.49
4063	CD	LXS A 634	57.432	-16.789	22.524	1.00	27.52
4064	CE	LXS A 634	57.239	-17.490	21.173	1.00	27.96
4065	NZ	LXS A 634	58.537	-17.479	20.413	1.00	29.38
4066	N	ILE A 635	55.768	-13.775	26.941	1.00	17.02
4067	CA	ILE A 635	56.142	-13.264	28.263	1.00	17.04
4068	C	ILE A 635	54.985	-13.581	29.221	1.00	18.26
4069	O	ILE A 635	55.242	-14.096	30.321	1.00	16.99
4070	CB	ILE A 635	56.444	-11.752	28.267	1.00	18.88
4071	CG1	ILE A 635	57.787	-11.462	27.535	1.00	18.51
4072	CG2	ILE A 635	56.370	-11.171	29.670	1.00	15.03
4073	CD1	ILE A 635	58.004	-9.955	27.358	1.00	18.80
4074	N	SER A 636	53.742	-13.211	28.818	1.00	16.75
4075	CA	SER A 636	52.587	-13.505	29.684	1.00	16.38
4076	C	SER A 636	4076				
4077	O	SER A 636	4077				
4078	CB	SER A 636	4078				
4079	OG	SER A 636	4079				
4080	N	ASN A 637	4080				
4081	CA	ASN A 637	4081				
4082	C	ASN A 637	4082				
4083	O	ASN A 637	4083				
4084	CB	ASN A 637	4084				
4085	CG	ASN A 637	4085				
4086	OD1	ASN A 637	4086				
4087	ND2	ASN A 637	4087				
4088	N	GLU A 638	4088				
4089	CA	GLU A 638	4089				
4090	C	GLU A 638	4090				
4091	O	GLU A 638	4091				
4092	CB	GLU A 638	4092				
4093	CG	GLU A 638	4093				
4094	CD	GLU A 638	4094				
4095	OE1	GLU A 638	4095				
4096	OE2	GLU A 638	4096				
4097	N	LEU A 639	4097				
4098	CA	LEU A 639	4098				
4099	C	LEU A 639	4099				
4100	O	LEU A 639	4100				
4101	CB	LEU A 639	4101				
4102	CG	LEU A 639	4102				
4103	CD1	LEU A 639	4103				
4104	CD2	LEU A 639	4104				
4105	N	HIS A 640	4105				
4106	CA	HIS A 640	4106				
4107	C	HIS A 640	4107				
4108	O	HIS A 640	4108				
4109	CB	HIS A 640	4109				
4110	CG	HIS A 640	4110				
4111	ND1	HIS A 640	4111				
4112	CD2	HIS A 640	4112				
4113	CE1	HIS A 640	4113				
4114	NE2	HIS A 640	4114				
4115	N	ALA A 641	4115				
4116	CA	ALA A 641	4116				
4117	C	ALA A 641	4117				
4118	O	ALA A 641	4118				
4119	CB	ALA A 641	4119				
4120	N	ILE A 642	4120				
4121	CA	ILE A 642	4121				
4122	C	ILE A 642	4122				
4123	O	ILE A 642	4123				
4124	CB	ILE A 642	4124				
4125	CG1	ILE A 642	4125				
4126	CG2	ILE A 642	4126				
4127	CD1	ILE A 642	4127				
4128	N	ASN A 643	4128				
52.396			52.396	-14.985	29.963	1.00	17.44
52.268			52.268	-15.366	31.134	1.00	15.83
51.327			51.327	-12.920	29.022	1.00	17.93
50.145			50.145	-13.262	29.716	1.00	18.44
52.473			52.473	-15.869	28.956	1.00	18.57
52.375			52.375	-17.314	29.219	1.00	20.52
53.492			53.492	-17.878	30.092	1.00	21.51
53.154			53.154	-18.683	30.984	1.00	22.24
52.291			52.291	-18.099	27.902	1.00	19.88
51.013			51.013	-17.754	27.145	1.00	21.97
50.142			50.142	-17.046	27.666	1.00	23.68
50.868			50.868	-18.237	25.912	1.00	21.76
55.825			55.825	-17.997	29.901	1.00	19.30
55.668			55.668	-17.545	32.199	1.00	21.15
55.839			55.839	-18.358	33.122	1.00	19.31
57.218			57.218	-17.580	30.253	1.00	21.35
57.655			57.655	-18.382	29.023	1.00	22.98
59.094			59.094	-18.201	28.573	1.00	24.51
59.324			59.324	-18.637	27.404	1.00	24.01
59.978			59.978	-17.673	29.315	1.00	22.90
55.428			55.428	-16.257	32.402	1.00	18.27
55.291			55.291	-15.771	33.784	1.00	19.11
54.017			54.017	-16.268	34.422	1.00	19.62
54.073			54.073	-16.629	35.613	1.00	19.57
55.454			55.454	-14.237	33.905	1.00	17.12
56.786			56.786	-13.720	33.342	1.00	17.07
56.903			56.903	-12.195	33.297	1.00	15.55
57.975			57.975	-14.331	34.093	1.00	16.23
52.879			52.879	-16.404	33.716	1.00	19.06
51.679			51.679	-16.908	34.394	1.00	20.34
50.969			50.969	-18.816	35.671	1.00	21.35
50.420			50.420	-16.629	33.582	1.00	19.39
50.102			50.102	-15.160	33.517	1.00	20.54
50.217			50.217	-14.293	34.601	1.00	19.70
49.610			49.610	-14.433	32.483	1.00	18.57
49.752			49.752	-13.097	34.246	1.00	18.71
52.612			52.612	-13.172	32.965	1.00	19.82
52.801			52.801	-20.579	34.579	1.00	26.49
53.598			53.598	-20.615	35.882	1.00	27.89
53.510			53.510	-21.587	36.628	1.00	31.74
53.605			53.605	-21.327	33.512	1.00	26.50
54.437			54.437	-19.626	36.174	1.00	28.13
55.107			55.107	-19.555	37.476	1.00	29.40
54.093			54.093	-19.073	38.530	1.00	28.86
53.932			53.932	-19.665	39.596	1.00	26.64
56.310			56.310	-18.608	37.450	1.00	29.90
57.312			57.312	-18.997	36.344	1.00	30.38
57.009			57.009	-18.615	38.817	1.00	30.02
58.394			58.394	-17.943	36.170	1.00	30.48
53.361			53.361	-17.993	38.188	1.00	26.34

4129	CA	ASN A 643	52.345	-17.452	39.112	1.00	23.82	4182	N	GLY A 650	51.670	-2.046	29.915	1.00	18.09
4130	C	ASN A 643	51.282	-16.700	38.316	1.00	24.17	4183	CA	GLY A 650	52.684	-1.112	29.378	1.00	16.66
4131	O	ASN A 643	51.544	-15.628	37.774	1.00	21.45	4184	C	GLY A 650	52.088	-0.094	28.439	1.00	17.73
4132	CB	ASN A 643	53.051	-16.543	40.122	1.00	22.05	4185	O	GLY A 650	50.851	-0.034	28.270	1.00	16.48
4133	CG	ASN A 643	52.079	-15.861	41.083	1.00	23.41	4186	N	GLU A 651	52.922	0.800	27.876	1.00	17.53
4134	OD1	ASN A 643	50.871	-16.089	41.037	1.00	21.01	4187	CA	GLU A 651	52.431	1.880	27.026	1.00	17.39
4135	ND2	ASN A 643	52.555	-15.009	41.966	1.00	22.58	4188	C	GLU A 651	52.077	1.368	25.620	1.00	17.53
4136	N	PRO A 644	50.049	-17.213	38.277	1.00	23.33	4189	O	GLU A 651	52.976	0.899	24.910	1.00	19.12
4137	CA	PRO A 644	48.956	-16.613	37.531	1.00	22.06	4190	CB	GLU A 651	53.546	2.926	26.950	1.00	19.60
4138	C	PRO A 644	48.572	-15.222	37.983	1.00	19.69	4191	CG	GLU A 651	53.976	3.596	28.238	1.00	20.41
4139	O	PRO A 644	47.936	-14.499	37.220	1.00	20.72	4192	CD	GLU A 651	55.141	4.573	28.068	1.00	22.59
4140	CB	PRO A 644	47.775	-17.582	37.713	1.00	23.07	4193	OE1	GLU A 651	56.242	4.141	27.636	1.00	18.94
4141	CG	PRO A 644	48.101	-18.344	38.959	1.00	24.32	4194	OE2	GLU A 651	54.935	5.780	28.390	1.00	20.69
4142	CD	PRO A 644	49.621	-18.473	38.945	1.00	23.67	4195	N	PRO A 652	50.856	1.556	25.122	1.00	17.10
4143	N	GLY A 645	48.892	-14.797	39.190	1.00	18.01	4196	CA	PRO A 652	50.515	1.043	23.784	1.00	18.38
4144	CA	GLY A 645	48.637	-13.494	39.741	1.00	17.70	4197	C	PRO A 652	50.940	1.945	22.648	1.00	18.28
4145	C	GLY A 645	49.592	-12.380	39.283	1.00	19.60	4198	O	PRO A 652	50.125	2.221	21.773	1.00	19.43
4146	O	GLY A 645	50.660	-12.723	38.538	1.00	18.09	4199	CB	PRO A 652	48.957	0.908	23.883	1.00	17.61
4147	N	ILE A 646	51.643	-11.732	38.106	1.00	17.16	4200	CG	PRO A 652	48.591	2.087	24.748	1.00	16.44
4148	CA	ILE A 646	50.986	-10.704	37.203	1.00	16.23	4201	CD	PRO A 652	49.695	2.112	25.852	1.00	15.52
4149	C	ILE A 646	50.260	-11.076	36.307	1.00	17.07	4202	N	TRP A 653	52.098	2.594	22.614	1.00	18.69
4150	O	ILE A 646	52.885	-12.409	37.477	1.00	17.81	4203	CA	TRP A 653	52.549	3.503	21.554	1.00	18.43
4151	CB	ILE A 646	53.818	-12.981	38.569	1.00	18.48	4204	C	TRP A 653	54.075	3.398	21.359	1.00	17.97
4152	CG1	ILE A 646	53.723	-11.434	36.653	1.00	17.45	4205	O	TRP A 653	54.779	2.764	22.137	1.00	15.71
4153	CG2	ILE A 646	54.986	-13.812	37.398	1.00	16.75	4206	CB	TRP A 653	52.091	4.950	21.814	1.00	19.02
4154	CD1	ILE A 646	51.202	-9.403	37.398	1.00	16.03	4207	CG	TRP A 653	52.439	5.531	23.150	1.00	18.75
4155	N	VAL A 647	50.549	-8.329	36.668	1.00	15.29	4208	CD1	TRP A 653	53.659	5.991	23.523	1.00	20.11
4156	CA	VAL A 647	51.490	-7.688	35.644	1.00	16.91	4209	CD2	TRP A 653	51.603	5.706	24.308	1.00	20.38
4157	C	VAL A 647	52.608	-7.229	35.981	1.00	14.67	4210	NE1	TRP A 653	53.655	6.453	24.824	1.00	20.51
4158	O	VAL A 647	50.020	-7.276	37.651	1.00	16.53	4211	CE2	TRP A 653	52.378	6.290	25.318	1.00	20.60
4159	CB	VAL A 647	49.281	-6.165	36.945	1.00	15.28	4212	CE3	TRP A 653	50.242	5.446	24.554	1.00	19.16
4160	CG1	VAL A 647	49.094	-7.913	38.727	1.00	15.02	4213	CZ2	TRP A 653	51.869	6.584	26.595	1.00	22.37
4161	CG2	VAL A 647	51.048	-7.688	34.392	1.00	13.55	4214	CZ3	TRP A 653	50.542	6.323	26.813	1.00	20.77
4162	N	LEU A 648	51.862	-7.214	33.256	1.00	16.97	4215	CH2	TRP A 653	54.658	4.006	20.338	1.00	17.06
4163	CA	LEU A 648	51.149	-6.179	32.396	1.00	17.87	4216	N	THR A 654	56.072	4.010	20.058	1.00	18.41
4164	C	LEU A 648	49.993	-6.422	32.031	1.00	18.62	4217	CA	THR A 654	56.620	5.431	20.270	1.00	19.84
4165	O	LEU A 648	52.123	-8.454	32.390	1.00	14.99	4218	C	THR A 654	55.835	6.339	20.572	1.00	20.60
4166	CB	LEU A 648	52.778	-9.673	33.034	1.00	14.65	4219	O	THR A 654	55.438	3.591	18.608	1.00	19.02
4167	CG	LEU A 648	52.716	-10.926	32.153	1.00	12.97	4220	CB	THR A 654	56.438	4.691	17.734	1.00	18.49
4168	CD1	LEU A 648	54.247	-9.321	33.383	1.00	12.67	4221	OG1	THR A 654	56.079	2.359	18.174	1.00	16.83
4169	CD2	LEU A 648	51.744	-5.012	32.124	1.00	17.59	4222	CG2	THR A 654	55.687	2.359	18.174	1.00	16.83
4170	N	TYR A 649	51.053	-3.961	31.359	1.00	17.71	4223	N	GLY A 655	57.916	5.601	20.196	1.00	21.18
4171	CA	TYR A 649	52.086	-3.025	30.737	1.00	18.28	4224	CA	GLY A 655	58.633	6.858	20.389	1.00	21.26
4172	C	TYR A 649	53.272	-3.151	31.086	1.00	18.59	4225	O	GLY A 655	58.929	7.605	19.077	1.00	24.38
4173	O	TYR A 649	50.082	-3.164	32.269	1.00	14.25	4226	C	GLY A 655	58.912	6.896	18.002	1.00	22.39
4174	CB	TYR A 649	50.752	-2.654	33.527	1.00	13.60	4227	N	GLY A 656	59.178	6.896	18.002	1.00	22.39
4175	CG	TYR A 649	50.833	-3.456	34.665	1.00	14.53	4228	CA	GLY A 656	59.338	7.387	16.658	1.00	24.45
4176	CD1	TYR A 649	51.240	-1.358	33.610	1.00	11.51	4229	C	GLY A 656	58.840	6.337	15.661	1.00	25.22
4177	CD2	TYR A 649	51.501	-3.023	35.819	1.00	13.05	4230	O	GLY A 656	58.050	5.459	16.055	1.00	25.29
4178	CE1	TYR A 649	51.869	-0.891	34.758	1.00	13.13	4231	N	THR A 657	59.280	6.365	14.403	1.00	23.11
4179	CE2	TYR A 649	52.001	-1.743	35.853	1.00	14.34	4232	CA	THR A 657	58.848	5.425	13.380	1.00	23.56
4180	CZ	TYR A 649	52.639	-1.254	36.972	1.00	11.99	4233	C	THR A 657	59.546	4.082	13.588	1.00	22.19
4181	OH	TYR A 649						4234	O	THR A 657	60.759	4.098	13.820	1.00	20.73

4235	CB	THR A 657	59.256	5.972	11.983	1.00	26.11	4288	O	LEU A 665	50.488	-3.843	17.884	1.00	17.87
4236	OG1	THR A 657	58.698	7.292	11.803	1.00	27.58	4289	CB	LEU A 665	52.765	-2.046	16.656	1.00	20.03
4237	CG2	THR A 657	58.669	5.066	10.912	1.00	26.30	4290	CB	LEU A 665	53.973	-1.662	15.786	1.00	21.89
4238	N	SER A 658	58.846	2.963	13.574	1.00	22.05	4291	CD1	LEU A 665	53.709	-0.411	14.951	1.00	20.88
4239	CA	SER A 658	59.408	1.688	13.981	1.00	22.49	4292	CD2	LEU A 665	55.207	-1.501	16.668	1.00	22.05
4240	C	SER A 658	59.740	0.805	12.779	1.00	23.91	4293	N	VAL A 666	51.929	-3.519	19.533	1.00	18.78
4241	O	SER A 658	58.952	0.966	11.879	1.00	21.76	4294	CA	VAL A 666	50.885	-3.678	20.558	1.00	18.52
4242	CB	SER A 658	58.435	0.890	14.874	1.00	22.19	4295	C	VAL A 666	50.237	-2.321	20.883	1.00	19.69
4243	OG	SER A 658	59.035	-0.398	15.133	1.00	20.61	4296	O	VAL A 666	50.466	-1.789	21.955	1.00	17.22
4244	N	GLY A 659	60.747	-0.101	12.852	1.00	22.44	4297	CB	VAL A 666	51.359	-4.354	21.835	1.00	16.96
4245	CA	GLY A 659	60.886	-1.041	11.765	1.00	22.70	4298	CG1	VAL A 666	50.206	-4.834	22.723	1.00	19.29
4246	C	GLY A 659	59.939	-2.211	11.917	1.00	24.64	4299	CG2	VAL A 666	52.295	-5.532	21.529	1.00	14.78
4247	O	GLY A 660	59.836	-3.016	10.967	1.00	25.07	4300	N	THR A 667	49.290	-1.919	20.033	1.00	20.48
4248	N	LEU A 660	59.245	-2.383	13.049	1.00	22.82	4301	CA	THR A 667	48.502	-0.702	20.179	1.00	20.14
4249	CA	LEU A 660	58.349	-3.534	13.163	1.00	22.64	4302	C	THR A 667	47.197	-1.024	20.902	1.00	18.13
4250	C	LEU A 660	57.049	-3.271	12.408	1.00	24.58	4303	O	THR A 667	46.985	-2.227	21.117	1.00	16.98
4251	O	LEU A 660	56.462	-2.191	12.541	1.00	23.39	4304	CB	THR A 667	48.269	-0.014	18.814	1.00	21.55
4252	CB	LEU A 660	58.032	-3.798	14.656	1.00	21.87	4305	OG1	THR A 667	47.843	-1.044	17.925	1.00	20.10
4253	CG	LEU A 660	57.221	-5.073	14.921	1.00	21.46	4306	CG2	THR A 667	49.597	0.611	18.281	1.00	21.18
4254	CD1	LEU A 660	58.005	-6.333	14.553	1.00	21.53	4307	N	LYS A 668	46.331	-0.058	21.255	1.00	16.86
4255	CD2	LEU A 660	56.796	-5.118	16.387	1.00	22.01	4308	CA	LYS A 668	45.140	-0.468	22.022	1.00	18.52
4256	N	SER A 661	56.498	-4.299	11.768	1.00	28.28	4309	C	LYS A 668	44.229	-1.401	21.234	1.00	19.25
4257	CA	SER A 661	55.249	-4.110	11.039	1.00	31.06	4310	O	LYS A 668	43.936	-1.077	20.104	1.00	15.25
4258	C	SER A 661	54.123	-3.721	11.988	1.00	31.92	4311	CB	LYS A 668	44.277	0.724	22.546	1.00	17.82
4259	O	SER A 661	53.977	-4.115	13.149	1.00	30.73	4312	CG	LYS A 668	45.148	1.580	23.472	1.00	19.27
4260	CB	SER A 661	54.841	-5.369	10.278	1.00	33.28	4313	CD	LYS A 668	44.324	2.507	24.357	1.00	22.35
4261	OG	SER A 661	54.406	-6.282	11.303	1.00	38.97	4314	CE	LYS A 668	43.581	3.587	23.574	1.00	22.93
4262	N	SER A 662	53.207	-2.944	11.425	1.00	31.42	4315	NZ	LYS A 668	44.581	4.231	22.654	1.00	24.34
4263	CA	SER A 662	52.040	-2.489	12.154	1.00	31.08	4316	N	GLY A 669	43.759	-2.439	21.897	1.00	20.04
4264	C	SER A 662	51.177	-3.592	12.719	1.00	30.70	4317	CA	GLY A 669	42.938	-3.451	21.239	1.00	20.82
4265	O	SER A 662	50.577	-3.441	13.808	1.00	29.15	4318	C	GLY A 669	43.782	-4.704	20.955	1.00	21.65
4266	CB	SER A 662	51.250	-1.605	11.179	1.00	33.72	4319	O	GLY A 669	43.213	-5.800	20.927	1.00	21.36
4267	OG	SER A 662	50.239	-0.982	11.936	1.00	37.74	4320	N	GLN A 670	45.088	-4.594	20.719	1.00	20.53
4268	N	ASP A 663	51.069	-4.738	12.047	1.00	29.07	4321	CA	GLN A 670	45.919	-5.759	20.428	1.00	21.35
4269	CA	ASP A 663	50.244	-5.830	12.522	1.00	30.96	4322	C	GLN A 670	46.297	-6.586	21.642	1.00	20.10
4270	C	ASP A 663	50.781	-6.442	13.814	1.00	27.66	4323	O	GLN A 670	46.749	-7.720	21.456	1.00	19.47
4271	O	ASP A 663	50.053	-7.210	14.429	1.00	24.98	4324	CB	GLN A 670	47.247	-5.387	19.714	1.00	21.19
4272	CB	ASP A 663	50.219	-6.998	11.510	1.00	37.98	4325	CG	GLN A 670	46.970	-4.705	18.368	1.00	27.47
4273	CG	ASP A 663	50.022	-6.418	10.118	1.00	43.25	4326	CD	GLN A 670	46.169	-5.614	17.439	1.00	31.69
4274	OD1	ASP A 663	51.041	-6.067	9.479	1.00	46.25	4327	OE1	GLN A 670	46.616	-6.684	17.021	1.00	32.50
4275	OD2	ASP A 663	48.826	-6.288	9.774	1.00	46.03	4328	NE2	GLN A 670	44.937	-5.233	17.073	1.00	34.39
4276	N	GLN A 664	52.066	-6.234	14.108	1.00	22.67	4329	N	GLN A 671	45.972	-6.145	22.858	1.00	19.44
4277	CA	GLN A 664	52.601	-6.838	15.333	1.00	23.37	4330	CA	GLN A 671	46.228	-6.920	24.059	1.00	19.31
4278	C	GLN A 664	52.675	-5.789	16.432	1.00	22.24	4331	C	GLN A 671	45.108	-7.890	24.371	1.00	19.04
4279	O	GLN A 664	52.822	-6.210	17.585	1.00	19.91	4332	O	GLN A 671	45.181	-8.640	25.368	1.00	19.01
4280	CB	GLN A 664	53.947	-7.514	15.015	1.00	23.40	4333	CB	GLN A 671	46.423	-5.943	25.252	1.00	18.95
4281	CG	GLN A 664	53.799	-8.961	14.521	1.00	24.74	4334	CG	GLN A 671	45.140	-5.479	25.924	1.00	18.55
4282	CD	GLN A 664	53.177	-9.871	15.593	1.00	25.49	4335	CD	GLN A 671	44.177	-4.651	25.083	1.00	18.72
4283	OE1	GLN A 664	53.749	-9.992	16.703	1.00	24.23	4336	OE1	GLN A 671	42.932	-4.761	25.238	1.00	19.28
4284	NE2	GLN A 664	52.036	-10.506	15.305	1.00	23.12	4337	NE2	GLN A 671	44.667	-3.817	24.177	1.00	15.65
4285	N	LEU A 665	52.600	-4.486	16.125	1.00	19.96	4338	N	LYS A 672	43.957	-7.772	23.698	1.00	17.47
4286	CA	LEU A 665	52.740	-3.486	17.200	1.00	19.39	4339	CA	LYS A 672	42.772	-8.535	24.053	1.00	18.28
4287	C	LEU A 665	51.651	-3.648	18.238	1.00	18.71	4340	C	LYS A 672	43.062	-10.006	24.247	1.00	17.84



4341	O	LYS A 672	43.624	-10.599	23.339	1.00	17.28	14.468	3.996	28.753	1.00	16.69
4342	CB	LYS A 672	41.622	-8.448	23.030	1.00	21.13	44.612	5.491	28.529	1.00	16.69
4343	CG	LYS A 672	40.888	-7.108	22.987	1.00	22.83	44.157	6.287	29.363	1.00	15.66
4344	CD	LYS A 672	39.854	-7.147	22.145	1.00	20.41	43.205	3.658	29.584	1.00	15.17
4345	CE	LYS A 672	38.826	-6.074	22.145	1.00	30.84	41.905	4.021	28.891	1.00	16.39
4346	NZ	LYS A 672	37.962	-5.616	21.015	1.00	33.27	43.998	3.672	29.326	1.00	19.69
4347	N	GLY A 673	42.644	-10.575	25.384	1.00	17.84	40.786	4.799	27.835	1.00	13.35
4348	CA	GLY A 673	42.889	-11.973	25.692	1.00	16.83	41.946	5.905	27.392	1.00	15.34
4349	C	GLY A 673	44.324	-12.396	25.938	1.00	17.57	45.204	7.314	27.098	1.00	17.64
4350	O	GLY A 673	44.584	-13.612	26.132	1.00	16.87	45.322	7.925	26.684	1.00	15.96
4351	N	LEU A 674	45.337	-11.535	26.003	1.00	16.05	43.983	9.146	26.750	1.00	18.29
4352	CA	LEU A 674	46.707	-12.002	26.224	1.00	17.22	43.930	7.675	26.088	1.00	16.68
4353	C	LEU A 674	47.121	-12.089	27.692	1.00	18.69	46.434	6.929	24.779	1.00	20.08
4354	O	LEU A 674	48.214	-12.614	27.992	1.00	16.27	46.314	5.745	24.708	1.00	18.82
4355	CB	LEU A 674	47.688	-11.070	25.482	1.00	16.47	45.917	7.570	23.728	1.00	21.03
4356	CG	LEU A 674	47.491	-10.955	23.957	1.00	17.85	46.590	7.183	26.388	1.00	16.19
4357	CD1	LEU A 674	48.601	-10.153	23.292	1.00	17.96	42.939	7.732	26.064	1.00	16.30
4358	CD2	LEU A 674	47.402	-12.356	23.376	1.00	17.89	41.008	8.391	27.314	1.00	17.28
4359	N	GLY A 675	46.351	-11.448	28.580	1.00	17.76	41.008	9.554	27.320	1.00	16.98
4360	CA	GLY A 675	46.690	-11.447	29.992	1.00	18.55	40.543	6.629	25.496	1.00	15.40
4361	C	GLY A 675	47.533	-10.238	30.385	1.00	18.93	40.706	6.205	24.062	1.00	17.13
4362	O	GLY A 675	48.418	-10.331	31.244	1.00	18.34	41.010	6.815	23.416	1.00	16.74
4363	N	ILE A 676	47.527	-9.199	29.566	1.00	17.85	41.866	5.175	23.511	1.00	15.15
4364	CA	ILE A 676	48.279	-7.984	29.777	1.00	18.64	41.032	7.677	28.454	1.00	16.35
4365	C	ILE A 676	47.341	-6.773	29.627	1.00	17.75	40.470	8.220	29.694	1.00	16.07
4366	O	ILE A 676	46.311	-6.893	28.941	1.00	16.31	41.284	9.380	30.251	1.00	17.30
4367	CB	ILE A 676	49.479	-7.831	28.825	1.00	19.70	40.836	10.455	30.737	1.00	17.55
4368	CG1	ILE A 676	49.028	-7.552	27.392	1.00	20.32	40.228	7.122	30.748	1.00	16.73
4369	CG2	ILE A 676	50.426	-9.050	28.832	1.00	17.85	39.118	7.666	31.535	1.00	17.76
4370	CD1	ILE A 676	50.167	-7.324	26.394	1.00	17.85	41.474	6.693	31.535	1.00	13.77
4371	N	GLY A 677	47.751	-5.639	30.156	1.00	13.65	38.930	6.930	32.986	1.00	18.13
4372	CA	GLY A 677	47.021	-4.394	30.070	1.00	15.81	42.600	9.261	30.064	1.00	15.73
4373	C	GLY A 677	47.769	-3.254	29.403	1.00	16.01	43.514	10.306	30.488	1.00	16.66
4374	O	GLY A 677	48.991	-3.301	29.151	1.00	16.11	43.207	11.587	29.736	1.00	15.87
4375	N	VAL A 678	47.638	-2.172	29.079	1.00	15.57	43.115	12.677	30.317	1.00	16.71
4376	CA	VAL A 678	47.038	-1.027	28.427	1.00	15.53	44.976	9.857	30.262	1.00	18.05
4377	C	VAL A 678	47.199	0.251	29.119	1.00	16.70	45.952	10.905	30.788	1.00	20.35
4378	O	VAL A 678	46.014	0.364	29.518	1.00	18.08	47.222	11.054	30.003	1.00	26.33
4379	CB	VAL A 678	47.310	-0.949	26.919	1.00	14.79	47.113	11.061	28.560	1.00	30.02
4380	CG1	VAL A 678	47.819	-2.120	26.065	1.00	16.01	48.001	10.589	27.682	1.00	32.36
4381	CG2	VAL A 678	45.761	-0.920	26.704	1.00	15.88	49.205	10.033	27.964	1.00	33.59
4382	N	PHE A 679	48.111	1.185	29.240	1.00	12.93	47.644	10.673	26.404	1.00	33.28
4383	CA	PHE A 679	47.799	2.494	29.790	1.00	13.80	43.193	11.515	28.410	1.00	15.54
4384	C	PHE A 679	46.705	3.036	28.866	1.00	16.99	42.944	12.721	27.596	1.00	17.75
4385	O	PHE A 679	46.830	3.061	27.626	1.00	16.58	41.554	13.294	27.914	1.00	16.60
4386	CB	PHE A 679	49.075	3.354	29.813	1.00	15.10	41.377	14.510	27.960	1.00	16.32
4387	CG	PHE A 679	49.992	3.064	30.997	1.00	16.37	43.101	12.404	26.078	1.00	15.79
4388	CD1	PHE A 679	51.234	2.485	30.823	1.00	17.10	44.559	12.204	25.670	1.00	17.29
4389	CD2	PHE A 679	49.591	3.420	32.282	1.00	15.14	45.564	12.731	26.189	1.00	15.27
4390	CE1	PHE A 679	52.097	2.258	31.903	1.00	17.80	44.757	11.357	24.661	1.00	18.75
4391	CE2	PHE A 679	50.451	3.191	33.364	1.00	17.84	40.581	12.454	28.172	1.00	16.82
4392	CZ	PHE A 679	51.687	2.594	33.195	1.00	16.20	39.208	12.841	28.482	1.00	18.79
4393	N	ASN A 680	45.614	3.469	29.502	1.00	17.15	39.085	13.538	29.825	1.00	18.90

447	O	GLY	A	686	38.321	14.506	29.982	1.00	18.03	4500	OD1	ASP	A	693	45.186	22.441	23.333	1.00	24.25
448	N	LEU	A	687	39.870	13.071	30.804	1.00	18.75	4501	OD2	ASP	A	693	47.013	23.154	24.306	1.00	23.36
449	CA	LEU	A	687	39.858	13.683	32.131	1.00	17.87	4502	N	LYS	A	694	49.301	21.803	26.426	1.00	22.37
450	C	LEU	A	687	40.445	15.084	32.155	1.00	19.56	4503	CA	LYS	A	694	49.397	22.197	27.836	1.00	26.78
4451	O	LEU	A	687	39.835	15.949	32.801	1.00	18.35	4504	C	LYS	A	694	48.227	23.020	28.342	1.00	25.75
4452	CB	LEU	A	687	40.553	12.740	33.143	1.00	17.50	4505	O	LYS	A	694	47.839	22.882	29.508	1.00	26.28
4453	CG	LEU	A	687	39.691	11.524	33.514	1.00	16.49	4506	CB	LYS	A	694	50.739	22.873	28.133	1.00	30.68
4454	CD1	LEU	A	687	40.525	10.497	34.266	1.00	15.82	4507	CG	LYS	A	694	50.740	24.392	28.133	1.00	30.68
4455	CD2	LEU	A	687	38.459	11.960	34.349	1.00	17.74	4508	CD	LYS	A	694	52.036	24.960	28.789	1.00	39.09
4456	N	ASP	A	688	41.590	15.386	31.529	1.00	19.00	4509	CE	LYS	A	694	52.086	26.494	28.763	1.00	41.48
4457	CA	ASP	A	688	42.114	16.743	31.606	1.00	19.09	4510	NZ	LYS	A	694	50.861	27.195	29.329	1.00	43.73
4458	C	ASP	A	688	42.632	17.315	30.289	1.00	18.61	4511	N	THR	A	695	47.560	23.824	27.511	1.00	23.27
4459	O	ASP	A	688	43.299	18.348	30.379	1.00	17.40	4512	CA	THR	A	695	46.427	24.909	27.898	1.00	24.00
4460	CB	ASP	A	688	43.247	16.843	32.624	1.00	21.76	4513	C	THR	A	695	45.407	23.936	27.789	1.00	21.80
4461	CG	ASP	A	688	44.491	16.033	32.362	1.00	20.12	4514	O	THR	A	695	44.094	24.597	28.158	1.00	23.18
4462	OD1	ASP	A	688	44.577	15.205	31.412	1.00	26.02	4515	CB	THR	A	695	46.289	25.932	27.057	1.00	26.17
4463	OD2	ASP	A	688	45.452	16.200	33.160	1.00	24.89	4516	OG1	THR	A	695	45.835	25.571	25.738	1.00	30.11
4464	N	GLY	A	689	42.237	16.788	29.143	1.00	19.33	4517	CG2	THR	A	695	47.536	26.727	27.038	1.00	26.32
4465	CA	GLY	A	689	42.679	17.411	27.872	1.00	20.12	4518	N	ALA	A	696	44.970	22.725	27.246	1.00	19.04
4466	C	GLY	A	689	43.852	16.650	27.244	1.00	18.25	4519	CA	ALA	A	696	43.034	21.799	28.438	1.00	18.20
4467	O	GLY	A	689	44.631	15.975	27.940	1.00	20.39	4520	C	ALA	A	696	43.750	21.502	29.404	1.00	18.12
4468	N	ASN	A	690	43.957	16.778	25.912	1.00	20.39	4521	O	ALA	A	696	43.747	20.900	26.195	1.00	18.13
4469	CA	ASN	A	690	45.008	16.103	25.159	1.00	18.52	4522	CB	ALA	A	696	40.214	20.039	29.320	1.00	19.35
4470	C	ASN	A	690	46.382	16.400	25.702	1.00	18.62	4523	N	GLN	A	697	40.935	20.340	29.647	1.00	17.77
4471	O	ASN	A	690	46.767	17.560	25.942	1.00	20.87	4524	CA	GLN	A	697	40.214	20.039	29.320	1.00	19.04
4472	CB	ASN	A	690	44.883	15.503	23.659	1.00	20.26	4525	C	GLN	A	697	40.134	19.653	28.146	1.00	18.13
4473	CA	ASN	A	690	45.899	15.668	22.877	1.00	22.43	4526	O	GLN	A	697	39.886	22.400	30.046	1.00	21.26
4474	OD1	ASN	A	690	47.036	16.114	22.664	1.00	22.38	4527	CB	GLN	A	697	39.886	22.400	30.046	1.00	21.26
4475	ND2	ASN	A	690	45.472	14.460	22.513	1.00	21.21	4528	CB	GLN	A	697	40.464	23.763	30.408	1.00	21.40
4476	N	VAL	A	691	47.256	15.408	25.828	1.00	17.79	4529	CD	GLN	A	697	39.454	24.837	30.803	1.00	23.53
4477	CA	VAL	A	691	48.582	15.528	26.410	1.00	20.26	4530	CD1	GLN	A	697	39.454	24.837	30.803	1.00	23.53
4478	C	VAL	A	691	49.536	16.419	25.616	1.00	20.63	4531	OE1	GLN	A	697	39.895	25.823	31.487	1.00	20.87
4479	O	VAL	A	691	50.503	16.940	26.182	1.00	19.98	4532	N	GLY	A	698	39.716	19.300	30.312	1.00	18.21
4480	CB	VAL	A	691	49.204	14.114	26.594	1.00	21.95	4533	CA	GLY	A	698	38.991	18.051	30.069	1.00	16.88
4481	CG1	VAL	A	691	49.485	13.451	25.233	1.00	19.94	4534	C	GLY	A	698	37.739	17.973	30.988	1.00	18.11
4482	CG2	VAL	A	691	50.487	14.150	27.404	1.00	21.70	4535	N	PHE	A	699	37.184	16.788	31.222	1.00	16.37
4483	N	PHE	A	692	49.287	16.668	24.331	1.00	19.63	4536	O	PHE	A	699	35.989	16.611	32.032	1.00	18.23
4484	CA	PHE	A	692	50.187	17.533	23.544	1.00	20.10	4537	CA	PHE	A	699	36.113	17.182	33.445	1.00	18.02
4485	C	PHE	A	692	49.799	19.008	23.561	1.00	18.56	4538	O	PHE	A	699	35.197	17.864	33.906	1.00	16.59
4486	CB	PHE	A	692	50.399	19.821	22.869	1.00	18.61	4539	C	PHE	A	699	35.608	15.121	32.107	1.00	17.98
4487	CG	PHE	A	692	50.238	17.053	22.090	1.00	18.53	4540	CB	PHE	A	699	34.419	14.751	32.963	1.00	18.86
4488	CD1	PHE	A	692	50.859	15.694	21.969	1.00	21.54	4541	CG	PHE	A	699	34.594	14.201	34.229	1.00	17.66
4489	CD2	PHE	A	692	50.085	14.538	21.907	1.00	20.75	4542	CD1	PHE	A	699	34.594	14.201	34.229	1.00	17.66
4490	CE1	PHE	A	692	52.245	15.579	21.964	1.00	21.43	4543	CD2	PHE	A	699	33.124	14.931	32.494	1.00	17.36
4491	CE2	PHE	A	692	50.723	13.309	21.812	1.00	21.57	4544	CE1	PHE	A	699	33.481	13.586	35.006	1.00	18.49
4492	CZ	PHE	A	692	52.865	14.348	21.891	1.00	21.34	4545	CE2	PHE	A	699	32.021	14.589	33.261	1.00	19.78
4493	N	ASP	A	693	52.097	13.205	21.793	1.00	21.14	4546	CZ	PHE	A	699	32.189	14.044	34.525	1.00	19.39
4494	CA	ASP	A	693	48.780	19.382	24.314	1.00	19.75	4547	N	ALA	A	700	37.233	16.927	34.136	1.00	16.55
4495	CB	ASP	A	693	48.307	20.760	24.442	1.00	18.18	4548	CA	ALA	A	700	37.367	17.425	35.495	1.00	16.01
4496	C	ASP	A	693	48.252	21.124	25.925	1.00	20.25	4549	C	ALA	A	700	37.613	18.922	35.560	1.00	17.98
4497	O	ASP	A	693	47.300	20.850	26.671	1.00	15.97	4550	O	ALA	A	700	37.438	19.479	36.654	1.00	16.39
4498	CB	ASP	A	693	46.932	20.849	23.734	1.00	20.28	4551	CB	ALA	A	700	38.547	16.728	36.197	1.00	15.97
4499	CG	ASP	A	693	46.336	22.240	23.779	1.00	22.51	4552	N	THR	A	701	38.066	19.547	34.474	1.00	17.35

4553	CA	THR A 701	38.531	20.920	34.525	1.00	18.55	4606	CB	ASP A 708	30.249	9.493	25.190	1.00	24.86
4554	C	THR A 701	37.744	21.889	33.629	1.00	19.85	4607	CG	ASP A 708	28.777	9.849	25.041	1.00	28.73
4555	O	THR A 701	38.226	23.004	33.458	1.00	20.14	4608	OD1	ASP A 708	27.911	9.562	25.888	1.00	29.20
4556	CB	THR A 701	40.027	21.044	34.148	1.00	18.45	4609	OD2	ASP A 708	28.457	10.460	24.000	1.00	32.49
4557	CG1	THR A 701	40.289	20.404	32.895	1.00	18.96	4610	N	VAL A 709	33.177	9.833	26.732	1.00	19.19
4558	CG2	THR A 701	40.941	20.438	35.213	1.00	19.17	4611	CA	VAL A 709	34.512	9.243	26.985	1.00	19.71
4559	N	GLY A 702	36.558	21.526	33.166	1.00	21.54	4612	C	VAL A 709	34.616	8.739	28.443	1.00	18.90
4560	CA	GLY A 702	35.692	22.478	32.466	1.00	23.96	4613	O	VAL A 709	35.086	7.622	28.734	1.00	16.65
4561	C	GLY A 702	35.279	22.206	31.039	1.00	24.73	4614	CB	VAL A 709	35.604	10.248	26.676	1.00	19.27
4562	O	GLY A 702	34.407	22.929	30.527	1.00	23.67	4615	CG1	VAL A 709	36.987	9.862	27.166	1.00	17.03
4563	N	ASP A 703	35.873	21.237	30.342	1.00	23.12	4616	CG2	VAL A 709	35.640	10.467	25.138	1.00	21.90
4564	CA	ASP A 703	35.398	20.922	28.991	1.00	23.82	4617	N	ILE A 710	34.165	9.578	29.376	1.00	17.70
4565	C	ASP A 703	34.070	20.187	29.093	1.00	23.19	4618	CA	ILE A 710	34.132	9.165	30.786	1.00	17.02
4566	O	ASP A 703	33.960	19.175	29.779	1.00	18.58	4619	C	ILE A 710	33.319	7.907	30.995	1.00	16.46
4567	CB	ASP A 703	36.431	20.071	28.241	1.00	23.36	4620	O	ILE A 710	33.789	6.942	31.644	1.00	15.43
4568	CG	ASP A 703	36.033	19.782	26.797	1.00	24.04	4621	CB	ILE A 710	33.641	10.356	31.640	1.00	16.39
4569	OD1	ASP A 703	36.618	20.476	25.930	1.00	25.71	4622	CG1	ILE A 710	34.615	11.533	31.483	1.00	19.18
4570	OD2	ASP A 703	35.188	18.926	26.500	1.00	21.20	4623	CG2	ILE A 710	33.543	9.944	33.100	1.00	16.50
4571	N	PRO A 704	33.059	20.609	28.324	1.00	24.11	4624	CD1	ILE A 710	36.090	11.238	31.712	1.00	15.64
4572	CA	PRO A 704	31.731	20.018	28.400	1.00	23.04	4625	N	LYS A 711	32.105	7.794	30.422	1.00	17.27
4573	C	PRO A 704	31.480	18.888	27.446	1.00	21.55	4626	CA	LYS A 711	31.267	6.607	30.613	1.00	17.74
4574	O	PRO A 704	30.401	18.265	27.492	1.00	21.23	4627	C	LYS A 711	31.972	5.347	30.102	1.00	17.56
4575	CB	PRO A 704	30.809	21.220	28.065	1.00	24.82	4628	O	LYS A 711	31.855	4.277	30.716	1.00	17.05
4576	CG	PRO A 704	31.633	21.977	27.058	1.00	25.35	4629	CB	LYS A 711	29.870	6.695	29.933	1.00	20.15
4577	CD	PRO A 704	33.080	21.823	27.468	1.00	24.45	4630	CG	LYS A 711	28.924	7.679	30.662	1.00	23.13
4578	N	ASN A 705	32.447	18.525	26.606	1.00	19.72	4631	CD	LYS A 711	27.567	7.592	29.962	1.00	28.41
4579	CA	ASN A 705	32.185	17.446	25.629	1.00	21.46	4632	CE	LYS A 711	26.580	8.731	30.447	1.00	30.81
4580	C	ASN A 705	32.802	16.090	25.927	1.00	23.27	4633	NZ	LYS A 711	25.271	8.572	29.682	1.00	34.74
4581	O	ASN A 705	32.884	15.294	24.976	1.00	23.47	4634	N	ASN A 712	32.624	5.442	28.943	1.00	16.24
4582	CB	ASN A 705	32.745	17.969	24.290	1.00	21.14	4635	CA	ASN A 712	33.389	4.323	28.403	1.00	17.57
4583	CG	ASN A 705	32.042	19.276	23.915	1.00	23.28	4636	C	ASN A 712	34.537	3.949	29.358	1.00	16.07
4584	OD1	ASN A 705	30.818	19.366	24.062	1.00	23.01	4637	O	ASN A 712	34.819	2.758	29.543	1.00	16.07
4585	ND2	ASN A 705	32.790	20.256	23.491	1.00	24.52	4638	CB	ASN A 712	33.967	4.698	27.036	1.00	18.74
4586	N	GLN A 706	33.030	15.688	27.187	1.00	21.97	4639	CG	ASN A 712	33.031	4.342	25.891	1.00	21.96
4587	CA	GLN A 706	33.650	14.375	27.459	1.00	21.06	4640	OD1	ASN A 712	32.812	3.181	25.595	1.00	21.32
4588	C	GLN A 706	32.804	13.352	28.193	1.00	21.75	4641	ND2	ASN A 712	32.322	5.338	25.353	1.00	23.31
4589	O	GLN A 706	33.297	12.317	28.660	1.00	20.03	4642	N	GLY A 713	35.160	4.910	30.029	1.00	15.84
4590	CB	GLN A 706	34.918	14.683	28.310	1.00	20.55	4643	CA	GLY A 713	36.196	4.574	31.026	1.00	15.68
4591	CG	GLN A 706	35.854	15.729	27.750	1.00	19.45	4644	C	GLY A 713	35.616	3.941	32.302	1.00	16.62
4592	CD	GLN A 706	36.345	15.354	26.363	1.00	23.83	4645	O	GLY A 713	36.235	3.026	32.905	1.00	15.22
4593	OE1	GLN A 706	36.610	14.155	26.140	1.00	24.34	4646	N	VAL A 714	34.458	4.434	32.755	1.00	16.34
4594	NE2	GLN A 706	36.463	16.280	25.413	1.00	22.80	4647	CA	VAL A 714	33.775	3.909	33.951	1.00	15.53
4595	N	VAL A 707	31.486	13.514	28.358	1.00	20.98	4648	C	VAL A 714	33.490	2.430	33.793	1.00	15.76
4596	CA	VAL A 707	30.608	12.590	29.043	1.00	21.61	4649	O	VAL A 714	33.610	1.702	34.794	1.00	16.34
4597	C	VAL A 707	30.703	11.153	29.314	1.00	23.14	4650	CB	VAL A 714	32.457	4.629	34.258	1.00	16.87
4598	O	VAL A 707	30.863	10.217	29.304	1.00	19.91	4651	CG1	VAL A 714	31.474	3.887	35.168	1.00	14.77
4599	CB	VAL A 707	29.115	13.027	29.034	1.00	22.13	4652	CG2	VAL A 714	32.705	5.999	34.927	1.00	16.03
4600	CG1	VAL A 707	28.133	11.953	29.488	1.00	18.96	4653	N	ILE A 715	33.060	1.928	32.632	1.00	16.13
4601	CG2	VAL A 707	28.930	14.204	30.014	1.00	20.82	4654	CA	ILE A 715	32.769	0.468	32.556	1.00	15.59
4602	N	ASP A 708	30.635	10.964	27.180	1.00	23.14	4655	C	ILE A 715	34.003	-0.389	32.207	1.00	16.37
4603	CA	ASP A 708	30.701	9.604	26.647	1.00	22.35	4656	O	ILE A 715	33.911	-1.557	31.784	1.00	14.09
4604	C	ASP A 708	32.118	9.026	26.784	1.00	20.35	4657	CB	ILE A 715	31.619	0.207	31.554	1.00	15.72
4605	O	ASP A 708	32.175	7.813	26.913	1.00	18.36	4658	CG1	ILE A 715	31.997	0.689	30.136	1.00	15.41

4659	CG2	ILE A 715	30.315	0.959	31.967	1.00	15.73	4712	OG1	THR A 722	38.074	-3.670	28.117	1.00	16.78
4660	CD1	ILE A 715	30.904	0.480	29.056	1.00	17.76	4713	CG2	THR A 722	40.327	-2.847	27.866	1.00	14.81
4661	N	GLY A 716	35.234	0.099	32.413	1.00	15.99	4714	N	SER A 723	38.634	-6.684	26.382	1.00	20.49
4662	CA	GLY A 716	36.440	-0.726	32.202	1.00	14.94	4715	CA	SER A 723	37.652	-7.760	26.508	1.00	20.59
4663	C	GLY A 716	36.808	-0.841	30.730	1.00	15.94	4716	C	SER A 723	37.348	-8.047	27.978	1.00	19.48
4664	O	GLY A 716	37.424	-1.833	30.314	1.00	16.36	4717	O	SER A 723	36.524	-8.903	28.269	1.00	18.62
4665	N	SER A 717	36.394	0.105	29.882	1.00	13.02	4718	CB	SER A 723	38.180	-9.078	25.911	1.00	24.40
4666	CA	SER A 717	36.785	0.122	28.471	1.00	15.05	4719	OG	SER A 723	38.237	-8.849	24.496	1.00	30.69
4667	C	SER A 717	36.284	-1.033	27.650	1.00	15.07	4720	N	ALA A 724	38.066	-7.402	28.893	1.00	18.21
4668	O	SER A 717	36.690	-1.154	26.479	1.00	15.88	4721	CA	ALA A 724	37.899	-7.608	30.343	1.00	19.12
4669	CB	SER A 717	38.379	0.196	28.479	1.00	12.88	4722	C	ALA A 724	38.520	-6.384	31.027	1.00	17.24
4670	OG	SER A 717	38.624	1.550	28.854	1.00	16.45	4723	O	ALA A 724	39.416	-5.778	30.461	1.00	14.91
4671	N	ILE A 718	35.335	-1.833	28.140	1.00	13.58	4724	CB	ALA A 724	38.614	-8.866	30.799	1.00	18.06
4672	CA	ILE A 718	34.833	-3.017	27.485	1.00	16.06	4725	N	PRO A 725	38.026	-5.999	32.198	1.00	16.70
4673	C	ILE A 718	34.018	-2.762	26.216	1.00	18.30	4726	CA	PRO A 725	38.492	-4.783	32.855	1.00	16.71
4674	O	ILE A 718	33.755	-3.690	25.423	1.00	17.12	4727	C	PRO A 725	39.952	-4.840	33.276	1.00	15.43
4675	CB	ILE A 718	33.972	-3.868	28.463	1.00	14.85	4728	O	PRO A 725	40.587	-3.775	33.366	1.00	14.10
4676	CG1	ILE A 718	32.705	-3.102	28.902	1.00	14.22	4729	CB	PRO A 725	37.489	-4.567	33.975	1.00	16.43
4677	CG2	ILE A 718	34.803	-4.358	29.641	1.00	13.95	4730	CB	PRO A 725	37.007	-5.964	34.298	1.00	16.92
4678	CD1	ILE A 718	31.759	-3.997	29.708	1.00	14.94	4731	CD	PRO A 725	36.921	-6.642	32.931	1.00	16.63
4679	N	GLN A 719	33.665	-1.511	25.966	1.00	20.52	4732	N	SER A 726	40.558	-6.013	33.429	1.00	14.30
4680	CA	GLN A 719	33.070	-1.148	24.677	1.00	23.41	4733	CA	SER A 726	41.982	-6.146	33.752	1.00	16.27
4681	C	GLN A 719	34.019	-0.262	23.894	1.00	22.29	4734	C	SER A 726	42.918	-5.644	32.664	1.00	17.17
4682	O	GLN A 719	33.605	0.413	22.972	1.00	21.69	4735	O	SER A 726	44.114	-5.417	32.923	1.00	16.54
4683	CB	GLN A 719	31.726	-0.410	24.905	1.00	25.15	4736	CB	SER A 726	42.327	-7.619	34.067	1.00	15.36
4684	CG	GLN A 719	30.710	-1.398	25.487	1.00	29.75	4737	OG	SER A 726	42.016	-8.458	32.938	1.00	16.05
4685	CD	GLN A 719	30.193	-2.454	24.535	1.00	33.47	4738	N	GLU A 727	42.424	-5.385	31.443	1.00	17.23
4686	OE1	GLN A 719	30.552	-2.581	23.370	1.00	34.39	4739	CA	GLU A 727	43.285	-4.934	30.337	1.00	15.75
4687	NE2	GLN A 719	29.279	-3.300	25.048	1.00	35.85	4740	C	GLU A 727	43.407	-3.427	30.227	1.00	16.68
4688	N	ASP A 720	35.274	-0.139	24.286	1.00	20.49	4741	O	GLU A 727	44.127	-2.965	29.335	1.00	16.11
4689	CA	ASP A 720	36.189	0.785	23.621	1.00	20.66	4742	CB	GLU A 727	42.733	-5.464	29.003	1.00	16.78
4690	C	ASP A 720	37.361	-0.033	23.088	1.00	20.80	4743	CG	GLU A 727	42.684	-7.007	28.978	1.00	15.52
4691	O	ASP A 720	37.521	-0.167	21.880	1.00	19.75	4744	CD	GLU A 727	41.939	-7.565	27.761	1.00	17.00
4692	CB	ASP A 720	36.604	1.845	24.680	1.00	21.05	4745	OE1	GLU A 727	41.381	-6.829	26.934	1.00	15.44
4693	CG	ASP A 720	37.535	2.895	24.139	1.00	23.81	4746	OE2	GLU A 727	41.889	-8.794	27.542	1.00	17.47
4694	OD1	ASP A 720	37.824	2.819	22.920	1.00	23.07	4747	N	THR A 728	42.758	-2.643	31.103	1.00	13.84
4695	OD2	ASP A 720	37.996	3.843	24.839	1.00	25.42	4748	CA	THR A 728	42.902	-1.194	30.999	1.00	15.17
4696	N	PHE A 721	38.162	-0.679	23.947	1.00	18.58	4749	C	THR A 728	43.571	-0.687	32.286	1.00	15.61
4697	CA	PHE A 721	39.268	-1.508	23.422	1.00	18.29	4750	O	THR A 728	43.030	-0.930	33.380	1.00	15.14
4698	C	PHE A 721	39.608	-2.722	24.262	1.00	19.42	4751	CB	THR A 728	41.587	-0.424	30.739	1.00	14.97
4699	O	PHE A 721	40.655	-3.321	23.961	1.00	18.82	4752	OG1	THR A 728	41.796	1.025	30.886	1.00	15.95
4700	CB	PHE A 721	40.557	-0.647	23.250	1.00	16.48	4753	CG2	THR A 728	40.515	-0.764	31.802	1.00	14.40
4701	CG	PHE A 721	40.983	0.029	24.520	1.00	16.11	4754	N	ILE A 729	44.667	0.062	32.166	1.00	14.75
4702	CD1	PHE A 721	40.487	1.297	24.909	1.00	13.99	4755	CA	ILE A 729	45.295	0.716	33.325	1.00	14.43
4703	CD2	PHE A 721	41.893	-0.659	25.356	1.00	17.14	4756	C	ILE A 729	44.727	2.155	33.337	1.00	15.83
4704	CE1	PHE A 721	40.966	1.833	26.081	1.00	14.66	4757	O	ILE A 729	45.145	2.937	32.453	1.00	17.36
4705	CE2	PHE A 721	42.282	-0.123	26.610	1.00	15.32	4758	CB	ILE A 729	46.818	0.776	33.179	1.00	15.12
4706	CZ	PHE A 721	41.772	1.078	26.959	1.00	14.52	4759	CG1	ILE A 729	47.417	-0.582	32.833	1.00	13.83
4707	N	THR A 722	38.806	-3.129	25.271	1.00	18.35	4760	CG2	ILE A 729	47.496	1.228	34.524	1.00	16.20
4708	CA	THR A 722	39.234	-4.301	26.048	1.00	18.71	4761	CD1	ILE A 729	47.025	-1.766	33.724	1.00	11.75
4709	C	THR A 722	38.256	-5.465	25.964	1.00	20.07	4762	N	ASN A 730	43.764	2.501	34.179	1.00	15.29
4710	O	THR A 722	37.131	-5.187	25.605	1.00	15.87	4763	CA	ASN A 730	43.155	3.831	34.153	1.00	16.11
4711	CB	THR A 722	39.370	-4.000	27.568	1.00	18.02	4764	C	ASN A 730	44.036	4.865	34.850	1.00	15.71

4765	O	ASN A 730	44.559	4.561	35.927	1.00	14.58	4818	OD1 ASP A 736	58.079	10.474	29.782	1.00	18.44
4766	CB	ASN A 730	41.764	3.781	34.807	1.00	16.99	4819	OD2 ASP A 736	56.639	8.828	29.769	1.00	19.23
4767	CG	ASN A 730	40.776	2.775	34.203	1.00	16.76	4820	N ASP A 737	55.648	14.149	31.055	1.00	19.40
4768	OD1	ASN A 730	39.932	2.076	34.846	1.00	17.80	4821	CA ASN A 737	54.827	15.353	31.031	1.00	19.79
4769	ND2	ASN A 730	40.923	2.747	32.900	1.00	14.18	4822	C ASN A 737	54.651	15.987	32.411	1.00	20.31
4770	N	TYR A 731	44.303	6.022	34.261	1.00	14.78	4823	O ASN A 737	55.545	15.914	32.270	1.00	18.64
4771	CA	TYR A 731	45.135	7.013	34.912	1.00	16.43	4824	CB ASN A 737	53.499	15.028	30.295	1.00	20.11
4772	C	TYR A 731	44.889	8.442	34.401	1.00	16.53	4825	CG ASN A 737	53.794	14.336	28.972	1.00	20.21
4773	O	TYR A 731	44.321	8.554	33.309	1.00	16.09	4826	OD1 ASN A 737	53.500	13.160	28.760	1.00	23.28
4774	CB	TYR A 731	46.641	6.738	34.752	1.00	16.77	4827	ND2 ASN A 737	54.473	14.985	28.022	1.00	20.26
4775	CG	TYR A 731	47.189	6.951	33.358	1.00	17.72	4828	N MET A 738	53.530	16.651	32.711	1.00	19.26
4776	CD1	TYR A 731	48.208	7.865	33.101	1.00	18.91	4829	CA MET A 738	53.389	17.416	33.938	1.00	19.59
4777	CD2	TYR A 731	46.723	6.190	32.306	1.00	16.97	4830	C MET A 738	52.657	16.709	35.085	1.00	19.41
4778	CE1	TYR A 731	48.689	8.074	31.810	1.00	20.50	4831	O MET A 738	51.854	15.813	34.846	1.00	17.92
4779	CE2	TYR A 731	47.152	6.393	31.015	1.00	19.21	4832	CB MET A 738	52.619	18.711	33.619	1.00	20.83
4780	CZ	TYR A 731	48.157	7.321	30.782	1.00	22.10	4833	CG MET A 738	53.300	19.598	32.561	1.00	22.68
4781	OH	TYR A 731	48.585	7.473	29.473	1.00	22.66	4834	SD MET A 738	52.260	21.070	32.188	1.00	25.13
4782	N	VAL A 732	45.463	9.396	35.150	1.00	14.45	4835	CE MET A 738	52.683	22.154	33.456	1.00	22.07
4783	CA	VAL A 732	45.429	10.782	34.652	1.00	15.94	4836	N THR A 739	52.939	17.124	36.311	1.00	17.76
4784	C	VAL A 732	46.793	11.401	34.486	1.00	15.92	4837	CA THR A 739	52.155	16.614	37.447	1.00	18.00
4785	O	VAL A 732	46.949	12.340	33.663	1.00	16.20	4838	C THR A 739	50.770	17.275	37.332	1.00	18.02
4786	CB	VAL A 732	44.507	11.667	35.541	1.00	16.99	4839	O THR A 739	50.609	18.312	36.672	1.00	18.06
4787	CG1	VAL A 732	44.997	11.697	36.988	1.00	13.37	4840	CB THR A 739	52.781	16.952	38.809	1.00	19.29
4788	CG2	VAL A 732	44.444	13.123	35.006	1.00	17.23	4841	OG1 THR A 739	52.642	18.358	39.103	1.00	17.62
4789	N	THR A 733	47.822	11.034	35.242	1.00	15.69	4842	CG2 THR A 739	54.267	16.607	38.889	1.00	17.97
4790	CA	THR A 733	49.189	11.535	35.142	1.00	16.13	4843	N LEU A 740	49.739	16.694	37.916	1.00	16.11
4791	C	THR A 733	50.244	10.428	35.359	1.00	16.11	4844	CA LEU A 740	48.403	17.232	37.843	1.00	17.22
4792	O	THR A 733	49.918	9.357	35.898	1.00	13.88	4845	C LEU A 740	48.315	18.636	38.430	1.00	16.52
4793	CB	THR A 733	49.597	12.657	36.115	1.00	17.42	4846	O LEU A 740	47.642	19.447	37.769	1.00	17.44
4794	CG1	THR A 733	49.438	12.231	37.477	1.00	15.92	4847	CB LEU A 740	47.300	16.323	38.417	1.00	15.94
4795	CG2	THR A 733	48.827	13.958	35.888	1.00	14.57	4848	CG LEU A 740	45.862	16.743	38.020	1.00	16.72
4796	N	SER A 734	51.504	10.693	34.974	1.00	16.76	4849	CD1 LEU A 740	45.757	16.769	36.484	1.00	16.81
4797	CA	SER A 734	52.607	9.753	35.168	1.00	16.69	4850	CD2 LEU A 740	44.836	15.720	38.527	1.00	14.02
4798	C	SER A 734	53.925	10.520	35.190	1.00	17.73	4851	N TRP A 741	48.917	18.934	39.557	1.00	16.04
4799	O	SER A 734	53.869	11.751	35.123	1.00	18.37	4852	CA TRP A 741	48.920	20.276	40.119	1.00	20.12
4800	CB	SER A 734	52.699	8.630	34.116	1.00	16.19	4853	C TRP A 741	49.452	21.316	39.117	1.00	20.10
4801	OG	SER A 734	53.031	9.220	32.839	1.00	17.55	4854	O TRP A 741	48.838	22.376	38.903	1.00	20.13
4802	N	HIS A 735	55.095	9.901	35.332	1.00	16.87	4855	CB TRP A 741	49.692	20.303	41.435	1.00	17.80
4803	CA	HIS A 735	56.355	10.627	35.335	1.00	18.13	4856	CG TRP A 741	49.450	21.549	42.242	1.00	18.78
4804	C	HIS A 735	56.582	11.454	34.067	1.00	18.58	4857	CD1 TRP A 741	50.376	22.463	42.644	1.00	20.16
4805	O	HIS A 735	57.307	12.484	34.165	1.00	20.77	4858	CD2 TRP A 741	48.169	22.020	42.713	1.00	18.03
4806	CB	HIS A 735	57.585	9.714	35.570	1.00	16.15	4859	NE1 TRP A 741	49.758	23.472	43.361	1.00	21.18
4807	CG	HIS A 735	57.897	8.867	34.358	1.00	16.14	4860	CB2 TRP A 741	48.395	23.219	43.395	1.00	20.56
4808	ND1	HIS A 735	57.309	7.621	34.171	1.00	13.70	4861	CB3 TRP A 741	46.866	21.539	42.591	1.00	17.60
4809	CD2	HIS A 735	58.707	9.141	33.286	1.00	14.91	4862	CZ2 TRP A 741	47.368	23.961	44.000	1.00	20.50
4810	CE1	HIS A 735	57.772	7.135	33.010	1.00	16.16	4863	CZ3 TRP A 741	45.827	22.277	43.159	1.00	17.86
4811	NE2	HIS A 735	58.586	8.039	32.480	1.00	16.01	4864	CH2 TRP A 741	46.083	23.467	43.857	1.00	19.81
4812	N	ASP A 736	56.069	11.050	32.912	1.00	18.06	4865	N ASP A 742	50.582	21.019	38.485	1.00	19.17
4813	CA	ASP A 736	56.221	11.847	31.698	1.00	18.55	4866	CA ASP A 742	51.203	21.880	37.484	1.00	19.35
4814	C	ASP A 736	55.296	13.073	31.785	1.00	19.59	4867	C ASP A 742	50.350	21.984	36.222	1.00	17.93
4815	O	ASP A 736	54.252	13.058	32.472	1.00	14.38	4868	O ASP A 742	50.146	23.081	35.724	1.00	16.62
4816	CB	ASP A 736	55.851	11.014	30.458	1.00	19.05	4869	CB ASP A 742	52.592	21.376	37.082	1.00	18.32
4817	CG	ASP A 736	56.916	10.045	29.971	1.00	19.36	4870	CG ASP A 742	53.612	21.544	38.183	1.00	18.67

4871	OD1	ASP	A	742	53.279	21.975	39.300	1.00	19.97	4871	N	SER	A	750	43.100	31.111	35.973	1.00	27.45
4872	OD2	ASP	A	742	54.794	21.167	38.023	1.00	18.27	4872	CA	SER	A	750	42.373	32.079	36.834	1.00	30.33
4873	N	LYS	A	743	49.809	20.860	35.768	1.00	19.25	4873	C	SER	A	750	41.454	31.439	37.876	1.00	30.12
4874	CA	LYS	A	743	48.930	20.830	34.597	1.00	20.46	4874	O	SER	A	750	40.824	32.153	38.673	1.00	28.54
4875	C	LYS	A	743	47.680	21.685	34.812	1.00	20.53	4875	CB	SER	A	750	41.708	33.101	35.932	1.00	30.51
4876	O	LYS	A	743	47.388	22.506	33.953	1.00	18.46	4876	OG	SER	A	750	40.743	32.469	35.086	1.00	33.66
4877	CB	LYS	A	743	48.540	19.395	34.234	1.00	19.12	4877	N	ASP	A	751	41.410	30.106	37.977	1.00	27.22
4878	CG	LYS	A	743	47.336	19.231	33.334	1.00	18.93	4878	CA	ASP	A	751	40.591	29.469	39.011	1.00	25.49
4879	CD	LYS	A	743	47.578	19.872	31.951	1.00	20.19	4879	C	ASP	A	751	41.317	29.534	40.356	1.00	23.90
4880	CE	LYS	A	743	46.198	20.097	31.314	1.00	18.13	4880	O	ASP	A	751	42.551	29.566	40.384	1.00	21.81
4881	NZ	LYS	A	743	46.312	20.465	29.877	1.00	16.42	4881	CB	ASP	A	751	40.251	28.035	38.640	1.00	25.71
4882	N	ILE	A	744	47.000	21.537	35.966	1.00	20.06	4882	CG	ASP	A	751	39.119	27.964	37.643	1.00	27.68
4883	CA	ILE	A	744	45.812	22.353	36.210	1.00	19.39	4883	OD1	ASP	A	751	38.017	28.510	37.899	1.00	29.06
4884	C	ILE	A	744	46.150	23.835	36.365	1.00	20.80	4884	OD2	ASP	A	751	39.317	27.350	36.581	1.00	27.19
4885	O	ILE	A	744	45.365	24.660	35.853	1.00	22.66	4885	N	THR	A	752	40.546	29.584	41.463	1.00	21.83
4886	CB	ILE	A	744	44.977	21.824	37.385	1.00	20.28	4886	CA	THR	A	752	41.159	29.653	42.779	1.00	20.72
4887	CG1	ILE	A	744	44.363	20.462	36.995	1.00	17.01	4887	C	THR	A	752	41.855	28.311	43.098	1.00	21.26
4888	CG2	ILE	A	744	43.850	22.807	37.780	1.00	18.88	4888	O	THR	A	752	41.582	27.259	42.500	1.00	19.88
4889	CD1	ILE	A	744	43.768	19.712	38.182	1.00	15.17	4889	CB	THR	A	752	40.151	29.916	43.915	1.00	20.18
4890	N	LEU	A	745	47.292	24.254	36.899	1.00	19.68	4890	OG1	THR	A	752	39.251	28.794	44.021	1.00	16.86
4891	CA	LEU	A	745	47.690	25.652	36.898	1.00	23.49	4891	CG2	THR	A	752	39.235	31.142	43.708	1.00	18.66
4892	C	LEU	A	745	47.839	26.228	35.465	1.00	24.82	4892	N	GLU	A	753	42.751	28.429	44.076	1.00	21.78
4893	O	LEU	A	745	47.471	27.398	35.201	1.00	23.41	4893	CA	GLU	A	753	43.429	27.308	44.672	1.00	23.03
4894	CB	LEU	A	745	49.072	25.836	37.976	1.00	24.77	4894	C	GLU	A	753	42.430	26.254	45.153	1.00	21.75
4895	CG	LEU	A	745	49.509	27.212	37.976	1.00	28.42	4895	O	GLU	A	753	42.616	25.067	44.834	1.00	19.13
4896	CD1	LEU	A	745	48.531	27.865	38.985	1.00	28.65	4896	CB	GLU	A	753	44.332	27.648	45.874	1.00	24.56
4897	CD2	LEU	A	745	50.857	27.244	38.702	1.00	29.02	4897	CG	GLU	A	753	45.287	26.501	46.181	1.00	28.93
4898	N	ALA	A	746	48.322	25.358	34.544	1.00	22.10	4898	OE1	GLU	A	753	46.304	26.813	47.238	1.00	33.40
4899	CA	ALA	A	746	48.486	25.844	33.172	1.00	21.79	4899	OE2	GLU	A	753	47.067	25.968	47.729	1.00	35.28
4900	C	ALA	A	746	47.184	25.938	32.398	1.00	21.61	4900	N	ALA	A	754	46.378	28.035	47.614	1.00	34.78
4901	O	ALA	A	746	47.055	26.813	31.530	1.00	21.69	4901	C	ALA	A	754	41.408	26.715	45.929	1.00	19.55
4902	CB	ALA	A	746	49.458	24.871	32.456	1.00	19.18	4902	CA	ALA	A	754	40.439	25.748	46.423	1.00	18.95
4903	N	SER	A	747	46.292	24.932	32.552	1.00	19.68	4903	C	ALA	A	754	39.776	25.048	45.242	1.00	18.59
4904	CA	SER	A	747	45.040	24.968	31.851	1.00	19.92	4904	O	ALA	A	754	39.434	23.831	45.331	1.00	16.89
4905	C	SER	A	747	44.016	25.873	32.565	1.00	20.35	4905	CB	ALA	A	754	39.358	26.388	47.347	1.00	17.73
4906	O	SER	A	747	43.053	26.199	31.881	1.00	19.89	4906	N	ASP	A	755	39.310	25.765	44.207	1.00	18.37
4907	CB	SER	A	747	44.372	23.594	31.621	1.00	19.80	4907	CA	ASP	A	755	38.675	25.066	43.077	1.00	17.43
4908	OG	SER	A	747	44.018	22.968	32.866	1.00	22.16	4908	C	ASP	A	755	39.646	24.137	42.339	1.00	18.14
4909	N	ASN	A	748	44.061	26.141	33.871	1.00	20.37	4909	O	ASP	A	755	39.290	23.031	41.834	1.00	18.30
4910	CA	ASN	A	748	42.972	26.892	34.557	1.00	20.69	4910	CB	ASP	A	755	38.025	26.070	42.112	1.00	19.81
4911	C	ASN	A	748	43.616	27.982	35.418	1.00	21.19	4911	CG	ASP	A	755	36.624	26.560	42.475	1.00	21.04
4912	O	ASN	A	748	43.508	28.025	36.658	1.00	22.97	4912	OD1	ASP	A	755	36.190	27.580	41.939	1.00	21.93
4913	CB	ASN	A	748	42.230	25.944	35.499	1.00	20.68	4913	OD2	ASP	A	755	35.899	25.957	43.290	1.00	21.94
4914	CG	ASN	A	748	41.301	24.953	34.831	1.00	21.99	4914	N	ARG	A	756	40.914	24.503	42.188	1.00	18.10
4915	OD1	ASN	A	748	40.043	25.156	34.923	1.00	24.93	4915	CA	ARG	A	756	41.891	23.655	41.478	1.00	16.46
4916	ND2	ASN	A	748	41.827	23.973	34.134	1.00	18.77	4916	C	ARG	A	756	42.146	22.409	42.341	1.00	16.36
4917	N	PRO	A	749	44.412	28.851	34.819	1.00	22.66	4917	O	ARG	A	756	42.201	21.306	41.780	1.00	14.27
4918	CA	PRO	A	749	45.192	29.825	35.564	1.00	24.77	4918	CB	ARG	A	756	43.168	24.439	41.108	1.00	17.08
4919	C	PRO	A	749	44.317	30.787	36.354	1.00	24.99	4919	CG	ARG	A	756	42.898	25.555	40.071	1.00	20.15
4920	O	PRO	A	749	44.780	31.208	37.413	1.00	28.37	4920	CD	ARG	A	756	44.176	26.286	39.593	1.00	21.05
4921	CB	PRO	A	749	46.076	30.507	34.506	1.00	23.57	4921	NE	ARG	A	756	44.408	27.330	40.496	1.00	22.58
4922	CG	PRO	A	749	45.240	30.423	33.269	1.00	25.06	4922	CZ	ARG	A	756	45.623	27.329	41.346	1.00	22.14
4923	CD	PRO	A	749	44.574	29.067	33.359	1.00	22.65	4923	NH1	ARG	A	756	46.474	26.353	41.521	1.00	22.42

4977	NH2	ARG	A	756	45.814	28.363	42.142	1.00	24.17	5030	C	ALA	A	763	40.440	12.248	38.843	1.00	13.98
4978	N	ILE	A	757	42.144	22.500	43.688	1.00	15.45	5031	O	ALA	A	763	40.245	11.182	38.264	1.00	14.29
4979	CA	ILE	A	757	42.170	21.297	44.521	1.00	15.56	5032	CB	ALA	A	763	41.186	14.252	39.991	1.00	15.43
4980	C	ILE	A	757	40.977	20.388	44.257	1.00	16.59	5033	N	HIS	A	764	41.107	12.268	39.991	1.00	13.75
4981	O	ILE	A	757	41.151	19.162	43.993	1.00	16.56	5034	CA	HIS	A	764	41.529	11.018	40.633	1.00	14.85
4982	CB	ILE	A	757	42.316	21.636	46.034	1.00	17.09	5035	C	HIS	A	764	40.340	10.203	41.116	1.00	15.09
4983	CG1	ILE	A	757	43.755	22.055	46.341	1.00	15.23	5036	O	HIS	A	764	40.318	8.959	41.071	1.00	14.64
4984	CG2	ILE	A	757	41.894	20.412	46.892	1.00	16.32	5037	CB	HIS	A	764	42.523	11.373	41.764	1.00	16.48
4985	CD1	ILE	A	757	44.008	22.725	47.668	1.00	16.53	5038	CG	HIS	A	764	43.881	11.820	41.290	1.00	16.16
4986	N	LYS	A	758	39.751	20.951	44.189	1.00	15.17	5039	ND1	HIS	A	764	44.861	10.897	40.931	1.00	17.78
4987	CA	LYS	A	758	38.587	20.110	43.886	1.00	17.48	5040	CD2	HIS	A	764	44.425	13.045	41.106	1.00	14.29
4988	C	LYS	A	758	38.686	19.381	42.557	1.00	16.06	5041	CE1	HIS	A	764	45.980	11.539	40.576	1.00	13.10
4989	O	LYS	A	758	38.285	18.211	42.451	1.00	15.89	5042	NE2	HIS	A	764	45.734	12.822	40.663	1.00	18.06
4990	CB	LYS	A	758	37.245	20.915	43.892	1.00	15.97	5043	N	ALA	A	765	39.263	10.853	41.598	1.00	14.85
4991	CG	LYS	A	758	36.909	21.285	45.349	1.00	18.80	5044	CA	ALA	A	765	38.050	10.167	42.039	1.00	15.19
4992	CD	LYS	A	758	35.437	21.596	45.583	1.00	19.89	5045	C	ALA	A	765	37.481	9.281	40.923	1.00	15.79
4993	CE	LYS	A	758	35.018	22.900	44.976	1.00	21.56	5046	O	ALA	A	765	36.976	8.170	41.144	1.00	15.86
4994	NZ	LYS	A	758	33.521	22.969	44.892	1.00	23.65	5047	CB	ALA	A	765	36.973	11.185	42.450	1.00	15.09
4995	N	MET	A	759	39.199	20.079	41.536	1.00	15.74	5048	N	VAL	A	766	37.426	9.768	39.691	1.00	15.11
4996	CA	MET	A	759	39.327	19.517	40.200	1.00	15.98	5049	CA	VAL	A	766	37.011	8.984	38.524	1.00	14.49
4997	C	MET	A	759	40.354	18.390	40.160	1.00	14.93	5050	C	VAL	A	766	37.969	7.801	38.348	1.00	15.68
4998	O	MET	A	759	40.113	17.359	39.550	1.00	16.46	5051	O	VAL	A	766	37.484	6.669	38.206	1.00	15.59
4999	CB	MET	A	759	39.733	20.623	39.208	1.00	17.07	5052	CB	VAL	A	766	36.967	9.813	37.215	1.00	14.83
5000	CG	MET	A	759	38.714	21.707	38.855	1.00	19.35	5053	CG1	VAL	A	766	36.639	8.953	35.976	1.00	13.21
5001	SD	MET	A	759	39.471	23.010	37.839	1.00	19.26	5054	CG2	VAL	A	766	35.898	10.921	37.371	1.00	13.49
5002	CE	MET	A	759	38.242	24.312	37.984	1.00	21.66	5055	N	VAL	A	767	39.295	8.026	38.448	1.00	15.32
5003	N	ASP	A	760	41.459	18.508	40.908	1.00	16.22	5056	CA	VAL	A	767	40.182	6.831	38.337	1.00	15.78
5004	CA	ASP	A	760	42.480	17.450	41.007	1.00	16.26	5057	C	VAL	A	767	39.874	5.778	39.405	1.00	16.72
5005	C	ASP	A	760	41.911	16.200	41.659	1.00	17.21	5058	O	VAL	A	767	39.783	4.553	39.099	1.00	16.35
5006	O	ASP	A	760	42.042	15.049	41.214	1.00	17.75	5059	CB	VAL	A	767	41.656	7.260	38.475	1.00	15.24
5007	CB	ASP	A	760	43.645	18.034	41.819	1.00	17.31	5060	CG1	VAL	A	767	42.610	6.067	38.588	1.00	13.41
5008	CG	ASP	A	760	44.913	17.214	41.946	1.00	17.03	5061	CG2	VAL	A	767	42.126	8.151	37.317	1.00	14.80
5009	OD1	ASP	A	760	44.793	15.983	42.065	1.00	15.47	5062	N	PHE	A	768	39.717	6.221	40.658	1.00	16.27
5010	OD2	ASP	A	760	46.047	17.756	41.909	1.00	14.89	5063	CA	PHE	A	768	39.471	5.305	41.772	1.00	16.07
5011	N	GLU	A	761	41.234	16.368	42.799	1.00	16.56	5064	C	PHE	A	768	38.094	4.659	41.812	1.00	16.53
5012	CA	GLU	A	761	40.568	15.332	43.536	1.00	16.85	5065	O	PHE	A	768	37.996	3.555	42.413	1.00	15.80
5013	C	GLU	A	761	39.469	14.695	42.670	1.00	16.63	5066	CB	PHE	A	768	39.838	5.868	43.137	1.00	15.94
5014	O	GLU	A	761	39.350	13.466	42.667	1.00	15.05	5067	CG	PHE	A	768	41.238	6.460	43.307	1.00	16.54
5015	CB	GLU	A	761	39.959	15.955	44.815	1.00	18.53	5068	CD1	PHE	A	768	41.402	7.676	43.923	1.00	15.00
5016	CG	GLU	A	761	40.986	16.290	45.884	1.00	17.58	5069	CD2	PHE	A	768	42.374	5.808	42.882	1.00	17.09
5017	CD	GLU	A	761	40.366	16.960	47.100	1.00	18.11	5070	CE1	PHE	A	768	42.654	8.258	44.120	1.00	16.04
5018	OEL	GLU	A	761	41.075	16.978	48.131	1.00	18.18	5071	CE2	PHE	A	768	43.640	6.366	43.042	1.00	17.04
5019	OE2	GLU	A	761	39.202	17.438	47.086	1.00	15.48	5072	CZ	PHE	A	768	43.783	7.583	43.673	1.00	16.63
5020	N	LEU	A	762	38.681	15.476	41.908	1.00	14.32	5073	N	THR	A	769	37.041	5.156	41.149	1.00	15.47
5021	CA	LEU	A	762	37.725	14.847	40.991	1.00	15.45	5074	CA	THR	A	769	35.736	4.475	41.230	1.00	14.36
5022	C	LEU	A	762	38.352	13.989	39.897	1.00	13.62	5075	C	THR	A	769	34.198	3.823	39.920	1.00	15.61
5023	O	LEU	A	762	37.806	12.922	39.595	1.00	13.44	5076	CB	THR	A	769	34.620	5.443	41.691	1.00	15.41
5024	CB	LEU	A	762	36.841	15.905	40.308	1.00	16.49	5077	CB	THR	A	769	34.713	6.617	40.902	1.00	14.96
5025	CG	LEU	A	762	35.804	15.442	39.294	1.00	20.45	5078	CG1	THR	A	769	34.762	5.855	43.174	1.00	15.33
5026	CD1	LEU	A	762	34.763	14.500	39.907	1.00	18.27	5079	CG2	THR	A	769	36.220	3.901	38.906	1.00	14.01
5027	CD2	LEU	A	762	35.059	16.623	38.651	1.00	20.38	5080	N	SR	A	770	35.921	3.261	37.631	1.00	14.16
5028	N	ALA	A	763	39.439	14.449	39.244	1.00	13.62	5081	CA	SR	A	770	35.921	3.261	37.631	1.00	14.16
5029	CA	ALA	A	763	40.002	13.575	38.205	1.00	14.02	5082	C	SR	A	770	36.302	1.788	37.682	1.00	14.69

5083	O	SER A 770	37.326	1.408	38.247	1.00	13.64	5136	CB	GLN A 777	52.175	10.388	39.136	1.00	15.88
5084	CB	SER A 770	36.746	3.878	36.481	1.00	14.15	5137	CG	GLN A 777	53.660	10.809	39.318	1.00	14.21
5085	CG	SER A 770	36.278	5.140	36.080	1.00	11.78	5138	CD	GLN A 777	54.081	12.028	38.491	1.00	16.72
5086	N	GLN A 771	35.626	0.960	36.880	1.00	13.77	5139	OE1	GLN A 777	55.294	12.354	38.396	1.00	15.28
5087	CA	GLN A 771	36.006	-0.422	36.664	1.00	13.99	5140	NE2	GLN A 777	53.132	12.777	37.931	1.00	13.34
5088	C	GLN A 771	37.356	-0.464	35.925	1.00	15.46	5141	N	GLY A 778	53.109	8.770	42.037	1.00	14.51
5089	O	GLN A 771	37.647	0.442	35.136	1.00	12.49	5142	CA	GLY A 778	53.354	8.968	43.469	1.00	12.51
5090	CB	GLN A 771	34.970	-1.223	35.849	1.00	13.53	5143	C	GLY A 778	53.552	10.434	43.782	1.00	15.81
5091	CG	GLN A 771	33.544	-1.161	36.443	1.00	13.08	5144	O	GLY A 778	54.236	11.120	42.976	1.00	16.75
5092	CD	GLN A 771	33.426	-1.789	37.822	1.00	14.69	5145	N	GLY A 779	52.939	10.912	44.890	1.00	14.32
5093	OE1	GLN A 771	32.830	-1.185	38.752	1.00	17.76	5146	CA	GLY A 779	53.108	12.345	45.197	1.00	14.20
5094	NE2	GLN A 771	33.956	-2.976	38.040	1.00	10.21	5147	C	GLY A 779	51.919	13.204	44.778	1.00	13.35
5095	N	GLY A 772	38.232	-1.456	36.210	1.00	15.16	5148	O	GLY A 779	51.774	14.341	45.263	1.00	13.40
5096	CA	GLY A 772	39.559	-1.446	35.598	1.00	14.97	5149	N	GLU A 780	51.027	12.713	43.910	1.00	12.45
5097	C	GLY A 772	40.698	-1.432	36.635	1.00	17.39	5150	CA	GLU A 780	49.829	13.482	43.533	1.00	12.05
5098	O	GLY A 772	40.444	-1.663	37.829	1.00	17.47	5151	C	GLU A 780	48.913	13.718	44.746	1.00	14.09
5099	N	VAL A 773	41.944	-1.109	36.210	1.00	14.33	5152	O	GLU A 780	48.336	14.808	44.855	1.00	15.37
5100	CA	VAL A 773	43.079	-1.067	37.150	1.00	14.45	5153	CB	GLU A 780	48.989	12.898	42.410	1.00	13.91
5101	C	VAL A 773	43.498	0.376	37.463	1.00	14.94	5154	CG	GLU A 780	49.577	12.770	41.025	1.00	16.76
5102	O	VAL A 773	44.084	0.998	36.611	1.00	16.35	5155	CD	GLU A 780	50.238	13.981	40.396	1.00	20.75
5103	CB	VAL A 773	44.310	-1.795	36.560	1.00	13.88	5156	OE1	GLU A 780	51.146	14.633	41.024	1.00	19.70
5104	CG1	VAL A 773	45.422	-1.889	37.632	1.00	14.66	5157	OE2	GLU A 780	49.891	14.243	39.214	1.00	19.72
5105	CG2	VAL A 773	44.005	-3.217	36.086	1.00	12.67	5158	N	GLU A 781	48.866	12.843	45.725	1.00	14.52
5106	N	PRO A 774	43.257	0.966	38.599	1.00	13.58	5159	CA	GLU A 781	48.154	12.941	46.974	1.00	15.90
5107	CA	PRO A 774	43.649	2.341	38.928	1.00	15.84	5160	C	GLU A 781	47.923	14.505	48.739	1.00	16.36
5108	C	PRO A 774	45.167	2.545	39.130	1.00	15.75	5161	O	GLU A 781	49.627	11.644	47.797	1.00	15.13
5109	O	PRO A 774	45.813	1.748	39.817	1.00	15.14	5162	CB	GLU A 781	48.261	11.644	47.797	1.00	16.08
5110	CB	PRO A 774	42.834	2.611	40.199	1.00	14.18	5163	CG	GLU A 781	49.627	11.402	48.399	1.00	16.18
5111	CG	PRO A 774	42.710	1.231	40.899	1.00	14.41	5164	CD	GLU A 781	50.695	10.808	47.504	1.00	16.18
5112	CD	PRO A 774	42.527	0.274	39.729	1.00	13.83	5165	OE1	GLU A 781	51.749	10.429	48.068	1.00	16.29
5113	N	PHE A 775	45.788	3.610	38.635	1.00	14.44	5166	OE2	GLU A 781	50.534	10.719	46.283	1.00	13.64
5114	CA	PHE A 775	47.368	5.379	39.009	1.00	15.10	5167	N	MET A 782	49.842	14.681	47.552	1.00	18.10
5115	C	PHE A 775	46.501	6.130	38.554	1.00	13.30	5168	CA	MET A 782	50.278	15.860	48.278	1.00	18.57
5116	O	PHE A 775	47.900	3.601	37.345	1.00	12.64	5169	C	MET A 782	50.588	17.012	47.311	1.00	18.29
5117	CB	PHE A 775	49.278	4.170	37.094	1.00	13.05	5170	O	MET A 782	51.393	17.853	47.652	1.00	19.99
5118	CG	PHE A 775	49.496	5.505	36.842	1.00	12.94	5171	CB	MET A 782	51.460	15.657	49.216	1.00	19.24
5119	CD1	PHE A 775	50.356	3.300	37.074	1.00	14.88	5172	CG	MET A 782	52.667	14.956	48.626	1.00	21.00
5120	CD2	PHE A 775	50.749	6.040	36.616	1.00	15.54	5173	SD	MET A 782	53.939	14.548	49.843	1.00	19.47
5121	CE1	PHE A 775	51.633	3.813	36.809	1.00	16.38	5174	CE	MET A 782	55.206	13.871	48.770	1.00	24.22
5122	CE2	PHE A 775	51.828	5.157	36.592	1.00	15.45	5175	N	LEU A 783	49.947	17.109	46.165	1.00	17.38
5123	CZ	PHE A 775	48.332	5.763	39.836	1.00	14.40	5176	CA	LEU A 783	50.155	18.163	45.193	1.00	18.72
5124	N	MET A 776	48.537	7.192	40.097	1.00	15.32	5177	C	LEU A 783	51.620	18.346	44.767	1.00	19.18
5125	CA	MET A 776	50.042	7.492	40.068	1.00	16.66	5178	O	LEU A 783	52.145	19.459	44.641	1.00	18.25
5126	C	MET A 776	50.796	6.561	40.340	1.00	16.26	5179	CB	LEU A 783	49.475	19.451	45.699	1.00	17.56
5127	O	MET A 776	47.999	7.642	41.453	1.00	14.34	5180	CG	LEU A 783	48.014	19.300	46.199	1.00	17.76
5128	CB	MET A 776	48.432	6.833	42.653	1.00	15.93	5181	CD1	LEU A 783	47.488	20.670	46.671	1.00	17.88
5129	CG	MET A 776	47.677	7.342	44.233	1.00	13.48	5182	CD2	LEU A 783	47.044	18.790	45.147	1.00	17.03
5130	SD	MET A 776	9.017	44.325	1.00	14.69	5183	N	ARG A 784	52.365	17.273	44.548	1.00	18.59	
5131	CE	MET A 776	48.304	9.017	44.325	1.00	14.69	5184	CA	ARG A 784	53.781	17.338	44.128	1.00	16.30
5132	N	GLN A 777	50.420	8.732	39.804	1.00	16.06	5185	C	ARG A 784	53.899	18.310	42.947	1.00	16.06
5133	CA	GLN A 777	51.838	9.108	39.931	1.00	15.06	5186	O	ARG A 784	53.105	18.204	42.016	1.00	13.00
5134	C	GLN A 777	52.082	9.345	41.420	1.00	13.74	5187	CB	ARG A 784	54.303	15.965	43.754	1.00	16.36
5135	O	GLN A 777	51.281	10.097	41.996	1.00	12.00	5188	CG	ARG A 784	55.732	15.937	43.128	1.00	15.05



5189	CD	ARG	A	784	56.414	14.612	43.471	1.00	14.37	5242	N	SER	A	792	61.156	15.862	32.889	1.00	18.66
5190	NE	ARG	A	784	57.508	14.212	42.581	1.00	15.11	5243	CA	SER	A	792	62.048	15.872	34.014	1.00	18.76
5191	CZ	ARG	A	784	57.463	13.745	41.344	1.00	15.42	5244	C	SER	A	792	63.218	14.927	34.077	1.00	17.02
5192	NH1	ARG	A	784	56.328	13.510	40.649	1.00	14.22	5245	O	SER	A	792	63.795	14.823	35.171	1.00	15.69
5193	NH2	ARG	A	784	58.620	13.430	40.733	1.00	14.18	5246	CB	SER	A	792	61.153	15.277	35.222	1.00	21.30
5194	N	THR	A	785	54.889	19.199	42.961	1.00	16.44	5247	OG	SER	A	792	60.809	16.404	35.929	1.00	26.39
5195	CA	THR	A	785	55.115	20.158	41.892	1.00	15.86	5248	N	TYR	A	793	63.515	14.156	33.037	1.00	17.61
5196	C	THR	A	785	56.506	20.037	41.278	1.00	17.13	5249	CA	TYR	A	793	64.461	13.062	33.084	1.00	19.03
5197	O	THR	A	785	57.501	19.843	41.965	1.00	17.03	5250	C	TYR	A	793	65.842	13.343	33.677	1.00	19.80
5198	CB	THR	A	785	54.867	21.626	42.325	1.00	16.69	5251	O	TYR	A	793	66.409	12.383	34.224	1.00	19.27
5199	OG1	THR	A	785	55.174	22.534	41.239	1.00	15.16	5252	CB	TYR	A	793	64.553	12.429	31.682	1.00	22.02
5200	CG2	THR	A	785	55.649	22.074	43.552	1.00	17.25	5253	CG	TYR	A	793	65.461	13.221	30.737	1.00	23.77
5201	N	LYS	A	786	56.614	20.188	39.958	1.00	18.17	5254	CD1	TYR	A	793	66.790	12.827	30.544	1.00	23.83
5202	CA	LYS	A	786	57.921	20.173	39.294	1.00	17.98	5255	CD2	TYR	A	793	64.965	14.342	30.075	1.00	22.77
5203	C	LYS	A	786	58.229	21.610	38.838	1.00	19.45	5256	CE1	TYR	A	793	67.610	13.552	29.690	1.00	24.44
5204	O	LYS	A	786	59.132	21.831	38.027	1.00	18.14	5257	CE2	TYR	A	793	65.776	15.058	29.210	1.00	24.72
5205	CB	LYS	A	786	57.889	19.233	38.073	1.00	16.77	5258	CZ	TYR	A	793	67.098	14.657	29.040	1.00	24.81
5206	CG	LYS	A	786	57.954	17.750	38.423	1.00	14.96	5259	OH	TYR	A	793	67.896	15.388	28.191	1.00	26.96
5207	CD	LYS	A	786	57.859	16.802	37.187	1.00	14.97	5260	N	ASN	A	794	66.476	14.496	33.547	1.00	19.42
5208	CE	LYS	A	786	57.877	15.352	37.713	1.00	15.19	5261	CA	ASN	A	794	67.801	14.743	34.132	1.00	22.06
5209	NZ	LYS	A	786	57.719	14.341	36.641	1.00	16.24	5262	C	ASN	A	794	67.762	16.039	34.931	1.00	22.30
5210	N	GLY	A	787	57.436	22.583	39.295	1.00	18.49	5263	O	ASN	A	794	68.798	16.678	35.115	1.00	22.69
5211	CA	GLY	A	787	57.644	23.974	38.910	1.00	20.70	5264	CB	ASN	A	794	68.903	14.841	33.039	1.00	25.15
5212	C	GLY	A	787	57.258	24.206	37.454	1.00	22.88	5265	CG	ASN	A	794	68.772	16.021	32.093	1.00	25.22
5213	O	GLY	A	787	57.860	25.094	36.818	1.00	23.87	5266	OD1	ASN	A	794	67.764	16.759	32.048	1.00	24.93
5214	N	GLY	A	788	56.399	23.347	36.861	1.00	21.35	5267	ND2	ASN	A	794	69.779	16.287	31.241	1.00	25.15
5215	CA	GLY	A	788	56.109	23.489	35.452	1.00	20.82	5268	N	ALA	A	795	66.383	17.734	36.035	1.00	20.96
5216	C	GLY	A	788	56.890	22.565	34.521	1.00	22.43	5270	C	ALA	A	795	66.819	17.900	37.481	1.00	20.75
5217	O	GLY	A	788	56.521	22.424	33.344	1.00	22.35	5271	O	ALA	A	795	66.796	19.075	37.914	1.00	20.75
5218	N	ASN	A	789	57.981	21.941	34.970	1.00	21.38	5272	CB	ALA	A	795	64.896	18.177	35.919	1.00	19.65
5219	CA	ASN	A	789	58.756	21.085	34.057	1.00	20.82	5273	N	GLY	A	796	67.107	16.854	38.225	1.00	18.52
5220	C	ASN	A	789	57.880	20.009	33.441	1.00	22.07	5274	CA	GLY	A	796	67.646	17.021	39.556	1.00	19.89
5221	O	ASN	A	789	59.929	20.450	34.788	1.00	21.85	5275	C	GLY	A	796	66.566	16.955	40.632	1.00	19.49
5222	CB	ASN	A	789	57.169	19.288	34.156	1.00	21.01	5276	O	GLY	A	796	65.390	16.814	40.694	1.00	18.74
5223	CB	ASN	A	789	61.082	20.034	33.891	1.00	21.99	5277	N	ASP	A	797	66.989	17.117	41.871	1.00	18.66
5224	OD1	ASN	A	789	62.224	20.457	34.093	1.00	23.49	5278	CA	ASP	A	797	66.128	16.903	43.044	1.00	20.03
5225	ND2	ASN	A	789	60.832	19.188	32.936	1.00	19.50	5279	C	ASP	A	797	65.167	18.013	43.367	1.00	21.02
5226	N	ASP	A	790	57.941	19.850	32.117	1.00	21.23	5280	O	ASP	A	797	63.994	17.803	43.701	1.00	20.32
5227	CA	ASP	A	790	57.167	18.811	31.470	1.00	22.38	5281	CB	ASP	A	797	67.067	16.594	44.244	1.00	19.80
5228	C	ASP	A	790	57.988	17.637	30.939	1.00	20.63	5282	CG	ASP	A	797	68.007	15.440	44.019	1.00	19.46
5229	O	ASP	A	790	57.393	16.915	30.142	1.00	19.94	5283	OD1	ASP	A	797	69.230	15.521	44.326	1.00	21.24
5230	CB	ASP	A	790	56.287	19.374	30.343	1.00	26.38	5284	OD2	ASP	A	797	67.633	14.351	43.526	1.00	20.79
5231	CG	ASP	A	790	57.068	19.930	29.177	1.00	30.47	5285	N	SER	A	798	65.560	19.280	43.210	1.00	21.85
5232	OD1	ASP	A	790	56.515	20.793	28.455	1.00	33.68	5286	CA	SER	A	798	64.685	20.423	43.474	1.00	28.03
5233	OD2	ASP	A	790	58.222	19.566	28.904	1.00	31.34	5287	C	SER	A	798	63.395	20.374	42.665	1.00	22.30
5234	N	ASN	A	791	59.253	17.444	31.796	1.00	19.26	5288	O	SER	A	798	62.323	20.682	43.172	1.00	19.63
5235	CA	ASN	A	791	60.065	16.323	30.796	1.00	20.27	5289	CB	SER	A	798	65.451	21.739	43.216	1.00	27.04
5236	C	ASN	A	791	61.345	16.285	31.637	1.00	21.29	5290	OG	SER	A	798	64.488	22.790	43.346	1.00	33.22
5237	O	ASN	A	791	62.427	16.809	31.319	1.00	21.30	5291	N	VAL	A	799	63.473	19.840	41.450	1.00	19.85
5238	CB	ASN	A	791	60.399	16.462	29.302	1.00	21.32	5292	CA	VAL	A	799	62.354	19.588	40.579	1.00	19.39
5239	CG	ASN	A	791	61.287	15.363	28.764	1.00	23.30	5293	C	VAL	A	799	61.603	18.281	40.867	1.00	19.66
5240	OD1	ASN	A	791	62.204	15.598	27.948	1.00	22.34	5294	O	VAL	A	799	60.379	18.346	40.925	1.00	18.31
5241	ND2	ASN	A	791	60.989	14.150	29.217	1.00	20.57										

5295	CB	VAL A 799	62.837	19.448	39.110	1.00	19.45	5348	N	SER A 805	57.047	18.260	53.210	1.00	21.38
5296	CG1	VAL A 799	61.707	19.105	38.147	1.00	17.83	5349	CA	SER A 805	56.412	19.375	53.886	1.00	21.85
5297	CG2	VAL A 799	63.547	20.738	38.692	1.00	20.77	5350	C	SER A 805	55.047	19.592	53.219	1.00	21.71
5298	N	ASN A 800	62.310	17.147	40.988	1.00	18.33	5351	O	SER A 805	54.135	20.065	53.884	1.00	23.61
5299	CA	ASN A 800	61.651	15.856	41.130	1.00	17.55	5352	CB	SER A 805	57.197	20.695	53.829	1.00	19.87
5300	C	ASN A 800	61.376	15.299	42.514	1.00	16.34	5353	OG	SER A 805	57.187	21.301	52.527	1.00	19.02
5301	O	ASN A 800	60.637	14.312	42.626	1.00	15.95	5354	N	ARG A 806	54.822	19.172	51.974	1.00	19.88
5302	CB	ASN A 800	62.512	14.802	40.393	1.00	17.74	5355	CA	ARG A 806	53.512	19.335	51.351	1.00	22.24
5303	CG	ASN A 800	62.543	14.987	38.883	1.00	19.36	5356	C	ARG A 806	52.442	18.396	51.883	1.00	21.51
5304	OD1	ASN A 800	63.584	15.273	38.249	1.00	20.67	5357	O	ARG A 806	51.254	18.722	51.750	1.00	19.94
5305	ND2	ASN A 800	61.404	14.856	38.247	1.00	17.72	5358	CB	ARG A 806	53.636	19.156	49.822	1.00	24.11
5306	N	GLN A 801	61.969	15.783	43.590	1.00	14.69	5359	CG	ARG A 806	54.034	20.543	49.260	1.00	26.24
5307	CA	GLN A 801	61.866	15.102	44.861	1.00	18.63	5360	CD	ARG A 806	54.401	20.399	47.801	1.00	24.25
5308	C	GLN A 801	60.471	15.071	45.487	1.00	16.56	5361	NE	ARG A 806	53.327	20.788	46.893	1.00	21.27
5309	O	GLN A 801	59.644	15.874	45.101	1.00	15.25	5362	CZ	ARG A 806	53.057	22.032	46.574	1.00	20.40
5310	CB	GLN A 801	62.806	15.707	45.932	1.00	17.66	5363	NH1	ARG A 806	53.779	23.031	47.094	1.00	21.72
5311	CG	GLN A 801	62.342	17.090	46.382	1.00	19.69	5364	NH2	ARG A 806	52.132	22.253	45.677	1.00	18.36
5312	CD	GLN A 801	63.483	17.927	46.966	1.00	21.59	5365	N	LYS A 807	52.841	17.251	52.437	1.00	20.38
5313	OE1	GLN A 801	64.500	17.414	47.435	1.00	22.85	5366	CA	LYS A 807	51.865	16.365	53.068	1.00	20.37
5314	NE2	GLN A 801	63.304	19.240	47.068	1.00	21.07	5367	C	LYS A 807	51.298	17.082	54.296	1.00	21.65
5315	N	PHE A 802	60.305	14.158	46.429	1.00	16.13	5368	O	LYS A 807	50.107	17.019	54.552	1.00	21.63
5316	CA	PHE A 802	59.071	14.118	47.240	1.00	18.33	5369	CB	LYS A 807	52.501	15.007	53.414	1.00	17.10
5317	C	PHE A 802	59.323	15.192	48.327	1.00	18.45	5370	CG	LYS A 807	51.504	14.093	54.081	1.00	18.69
5318	O	PHE A 802	60.112	14.942	49.246	1.00	19.38	5371	CE	LYS A 807	52.030	12.677	54.344	1.00	16.56
5319	CB	PHE A 802	58.763	12.759	47.875	1.00	16.57	5372	CD	LYS A 807	51.497	10.512	55.378	1.00	14.68
5320	CG	PHE A 802	58.053	11.737	47.006	1.00	19.68	5373	NZ	LYS A 807	52.112	17.787	55.077	1.00	20.44
5321	CD1	PHE A 802	58.287	11.656	45.645	1.00	18.62	5374	N	ALA A 808	51.606	18.577	56.202	1.00	23.20
5322	CD2	PHE A 802	57.109	10.859	47.565	1.00	20.70	5375	CA	ALA A 808	50.732	19.752	55.729	1.00	22.93
5323	CE1	PHE A 802	57.590	10.747	44.860	1.00	20.67	5376	C	ALA A 808	49.629	19.995	56.222	1.00	22.27
5324	CE2	PHE A 802	56.413	9.938	46.778	1.00	20.96	5377	O	ALA A 808	52.751	19.163	57.024	1.00	21.77
5325	CZ	PHE A 802	56.693	9.865	45.429	1.00	19.43	5378	CB	ALA A 808	51.188	20.477	54.706	1.00	23.89
5326	N	ASP A 803	58.624	16.288	48.253	1.00	18.57	5379	N	GLN A 809	50.492	21.617	54.146	1.00	20.32
5327	CA	ASP A 803	58.808	17.357	49.254	1.00	19.86	5380	CA	GLN A 809	49.162	21.215	53.507	1.00	23.43
5328	C	ASP A 803	57.793	17.081	50.357	1.00	20.28	5381	C	GLN A 809	51.356	22.355	53.095	1.00	25.14
5329	O	ASP A 803	56.641	17.492	50.205	1.00	19.15	5382	O	GLN A 809	48.168	21.944	53.608	1.00	20.37
5330	CB	ASP A 803	58.610	18.731	48.651	1.00	22.65	5383	CB	GLN A 809	51.547	24.361	51.551	1.00	29.36
5331	CG	ASP A 803	58.669	19.930	49.590	1.00	25.08	5384	CG	GLN A 809	50.627	23.521	52.421	1.00	26.75
5332	OD1	ASP A 803	58.806	19.685	50.814	1.00	25.27	5385	OE1	GLN A 809	52.735	24.031	51.422	1.00	28.08
5333	OD2	ASP A 803	58.588	21.104	49.167	1.00	23.70	5386	OE1	GLN A 809	51.050	25.449	50.941	1.00	30.28
5334	N	TRP A 804	58.233	16.380	51.405	1.00	18.05	5387	NE2	GLN A 809	49.159	20.078	52.774	1.00	22.26
5335	CA	TRP A 804	57.319	15.921	52.445	1.00	19.41	5388	N	PHE A 810	47.883	19.685	52.166	1.00	21.21
5336	C	TRP A 804	56.629	16.989	53.289	1.00	21.10	5389	CA	PHE A 810	47.375	18.387	52.769	1.00	21.19
5337	O	TRP A 804	55.653	16.669	53.993	1.00	19.44	5390	C	PHE A 810	46.913	17.517	52.055	1.00	20.62
5338	CB	TRP A 804	57.946	14.789	53.243	1.00	18.06	5391	O	PHE A 810	47.972	19.699	50.628	1.00	21.55
5339	CG	TRP A 804	58.290	13.537	52.497	1.00	19.31	5392	CB	PHE A 810	48.291	21.048	50.004	1.00	21.38
5340	CD1	TRP A 804	59.477	13.263	51.863	1.00	18.88	5393	CG	PHE A 810	49.557	21.281	49.481	1.00	20.93
5341	CD2	TRP A 804	57.474	12.380	52.297	1.00	19.81	5394	CD1	PHE A 810	47.348	22.067	49.928	1.00	21.54
5342	NE1	TRP A 804	59.448	12.034	51.283	1.00	18.40	5395	CD2	PHE A 810	49.832	22.549	48.923	1.00	22.85
5343	CE2	TRP A 804	58.216	11.461	51.531	1.00	18.59	5396	CE1	PHE A 810	47.627	23.285	49.368	1.00	21.34
5344	CE3	TRP A 804	56.163	12.061	52.677	1.00	18.95	5397	CE2	PHE A 810	48.881	23.543	48.856	1.00	22.67
5345	CZ2	TRP A 804	57.722	10.222	51.155	1.00	17.95	5398	CZ	PHE A 810	47.406	18.195	54.087	1.00	21.74
5346	CZ3	TRP A 804	55.674	10.809	52.304	1.00	18.76	5399	N	LYS A 811	46.912	16.982	54.753	1.00	21.92
5347	CH2	TRP A 804	56.437	9.922	51.551	1.00	17.47	5400	CA	LYS A 811					

5401	C	LYS A 811	45.455	16.673	54.422	1.00	21.36	5454	N	PHE A 817	42.434	11.487	49.320	1.00	12.51
5402	O	LYS A 811	45.136	15.481	54.277	1.00	17.59	5455	CA	PHE A 817	42.962	10.474	48.436	1.00	13.42
5403	CB	LYS A 811	47.062	17.024	56.289	1.00	23.82	5456	C	PHE A 817	42.911	9.109	49.162	1.00	13.97
5404	CG	LYS A 811	46.896	15.669	56.992	1.00	25.05	5457	O	PHE A 817	42.435	8.133	48.606	1.00	13.72
5405	CD	LYS A 811	47.863	14.620	56.452	1.00	27.06	5458	CB	PHE A 817	44.389	10.643	47.942	1.00	13.63
5406	CE	LYS A 811	48.035	13.364	57.285	1.00	27.83	5459	CG	PHE A 817	44.578	11.514	46.713	1.00	12.99
5407	NZ	LYS A 811	46.792	12.947	57.977	1.00	30.70	5460	CD1	PHE A 817	45.189	10.988	45.577	1.00	14.35
5408	N	ASP A 812	44.587	17.696	54.229	1.00	20.57	5461	CD2	PHE A 817	44.228	12.837	46.732	1.00	14.28
5409	CA	ASP A 812	43.212	17.388	53.835	1.00	21.91	5462	CE1	PHE A 817	45.442	11.773	44.444	1.00	14.16
5410	C	ASP A 812	43.149	16.742	52.456	1.00	20.65	5463	CE2	PHE A 817	44.474	13.644	45.615	1.00	15.25
5411	O	ASP A 812	42.273	15.900	52.246	1.00	18.27	5464	CZ	PHE A 817	45.056	13.124	44.486	1.00	14.04
5412	CB	ASP A 812	42.210	18.549	53.848	1.00	24.59	5465	N	SER A 818	43.376	9.113	50.407	1.00	12.87
5413	CG	ASP A 812	42.003	19.147	55.221	1.00	28.89	5466	CA	SER A 818	43.354	7.917	51.238	1.00	15.48
5414	OD1	ASP A 812	41.473	20.283	55.328	1.00	31.55	5467	C	SER A 818	41.955	7.389	51.512	1.00	14.72
5415	OD2	ASP A 812	42.371	18.534	56.241	1.00	28.92	5468	O	SER A 818	41.744	6.162	51.485	1.00	16.73
5416	N	VAL A 813	44.036	17.111	51.539	1.00	18.77	5469	CB	SER A 818	44.054	8.289	52.573	1.00	17.81
5417	CA	VAL A 813	44.040	16.444	50.227	1.00	18.35	5470	OG	SER A 818	43.841	7.176	53.431	1.00	22.91
5418	C	VAL A 813	44.516	15.007	50.355	1.00	16.42	5471	N	SER A 819	40.963	8.251	51.745	1.00	15.04
5419	O	VAL A 813	43.987	14.074	49.741	1.00	16.64	5472	CA	SER A 819	39.598	7.723	51.978	1.00	17.08
5420	CB	VAL A 813	44.922	17.275	49.264	1.00	19.35	5473	C	SER A 819	39.014	7.080	50.731	1.00	15.58
5421	CG1	VAL A 813	44.998	16.618	47.885	1.00	16.35	5474	O	SER A 819	38.311	6.062	50.828	1.00	15.56
5422	CG2	VAL A 813	44.486	18.742	49.166	1.00	19.07	5475	CB	SER A 819	38.630	8.852	52.401	1.00	18.73
5423	N	PHE A 814	45.548	14.793	51.166	1.00	16.24	5476	OG	SER A 819	39.098	9.381	53.642	1.00	18.88
5424	CA	PHE A 814	46.057	13.444	51.406	1.00	16.82	5477	N	MET A 820	39.241	7.652	49.551	1.00	16.10
5425	C	PHE A 814	44.943	12.573	51.982	1.00	17.46	5478	CA	MET A 820	39.374	5.710	48.019	1.00	18.57
5426	O	PHE A 814	47.296	11.422	51.542	1.00	17.98	5479	C	MET A 820	38.739	7.072	48.304	1.00	18.56
5427	CB	PHE A 814	47.209	13.524	52.431	1.00	16.63	5480	O	MET A 820	39.001	8.018	47.123	1.00	20.82
5428	CG	PHE A 814	47.862	12.187	52.659	1.00	16.39	5481	CB	MET A 820	38.153	7.749	45.900	1.00	23.16
5429	CD1	PHE A 814	49.038	11.891	51.984	1.00	16.20	5482	CG	MET A 820	36.405	8.041	45.961	1.00	22.93
5430	CD2	PHE A 814	47.296	11.269	53.540	1.00	16.49	5483	CE	MET A 820	36.118	9.783	45.834	1.00	23.13
5431	CE1	PHE A 814	49.633	10.652	52.204	1.00	17.12	5484	N	ILE A 821	40.688	5.642	48.244	1.00	17.40
5432	CE2	PHE A 814	47.896	10.030	53.752	1.00	18.46	5485	CA	ILE A 821	41.451	4.412	48.042	1.00	16.52
5433	CZ	PHE A 814	49.062	9.746	53.077	1.00	18.20	5486	C	ILE A 821	41.001	3.334	49.035	1.00	16.03
5434	N	ASP A 815	44.207	13.085	52.974	1.00	15.05	5487	O	ILE A 821	40.730	2.223	48.588	1.00	14.41
5435	CA	ASP A 815	43.133	12.307	53.595	1.00	17.46	5488	CB	ILE A 821	42.975	4.656	48.056	1.00	15.70
5436	C	ASP A 815	42.017	11.960	52.607	1.00	16.89	5489	CB	ILE A 821	43.474	5.516	46.885	1.00	13.40
5437	O	ASP A 815	41.334	10.919	52.706	1.00	19.94	5490	CG1	ILE A 821	43.644	3.255	48.054	1.00	15.43
5438	CB	ASP A 815	42.555	13.118	54.789	1.00	17.34	5491	CG2	ILE A 821	43.644	3.255	48.054	1.00	15.43
5439	CG	ASP A 815	43.531	13.119	55.974	1.00	20.48	5492	CD1	ILE A 821	44.782	6.262	47.154	1.00	11.03
5440	OD1	ASP A 815	44.579	12.408	55.987	1.00	19.52	5493	N	HIS A 822	40.778	3.678	50.314	1.00	14.76
5441	OD2	ASP A 815	43.252	13.962	56.862	1.00	21.01	5494	CA	HIS A 822	40.300	2.633	51.237	1.00	16.65
5442	N	TYR A 816	41.683	12.885	51.710	1.00	16.33	5495	C	HIS A 822	38.874	2.147	50.890	1.00	18.07
5443	CA	TYR A 816	40.663	12.564	50.678	1.00	16.00	5496	O	HIS A 822	38.504	0.977	51.044	1.00	16.15
5444	C	TYR A 816	41.171	11.496	49.742	1.00	15.70	5497	CB	HIS A 822	40.389	3.195	52.667	1.00	18.28
5445	O	TYR A 816	40.397	10.580	49.417	1.00	16.79	5498	CG	HIS A 822	41.797	3.237	53.209	1.00	18.71
5446	CB	TYR A 816	40.309	13.837	49.869	1.00	16.36	5499	ND1	HIS A 822	42.240	2.252	54.074	1.00	22.35
5447	CG	TYR A 816	39.217	13.680	48.824	1.00	15.25	5500	CD2	HIS A 822	42.825	4.101	53.055	1.00	17.41
5448	CD1	TYR A 816	39.444	13.129	47.564	1.00	15.93	5501	CE1	HIS A 822	43.525	2.504	54.403	1.00	19.56
5449	CD2	TYR A 816	37.918	14.077	49.117	1.00	15.92	5502	NE2	HIS A 822	43.884	3.652	53.816	1.00	20.90
5450	CE1	TYR A 816	38.400	12.970	46.633	1.00	15.05	5503	N	LEU A 823	38.009	3.101	50.498	1.00	14.46
5451	CE2	TYR A 816	36.886	13.958	48.209	1.00	16.61	5504	CA	LEU A 823	36.670	2.802	50.021	1.00	15.73
5452	CZ	TYR A 816	37.111	13.358	46.984	1.00	17.64	5505	C	LEU A 823	36.756	1.864	48.847	1.00	15.38
5453	OH	TYR A 816	36.060	13.227	46.088	1.00	19.15	5506	O	LEU A 823	36.209	0.707	49.030	1.00	15.40

5507	CB	LEU A 823	35.832	4.028	49.576	1.00	19.45	5560	CB	ALA A 829	30.396	-3.007	44.068	1.00	10.50
5508	CG	LEU A 823	34.486	3.700	49.019	1.00	21.92	5561	N	PHE A 830	33.342	-2.252	43.022	1.00	15.95
5509	CD1	LEU A 823	33.474	3.712	50.151	1.00	25.56	5562	CA	PHE A 830	34.152	-1.385	42.170	1.00	16.15
5510	CD2	LEU A 823	34.106	4.685	47.925	1.00	25.24	5563	C	PHE A 830	35.195	-2.117	41.342	1.00	16.91
5511	N	ARG A 824	37.475	2.025	47.744	1.00	14.25	5564	O	PHE A 830	35.922	-1.562	40.474	1.00	15.96
5512	CA	ARG A 824	37.617	0.995	46.740	1.00	13.61	5565	CB	PHE A 830	34.922	0.393	43.124	1.00	17.49
5513	C	ARG A 824	38.197	-0.307	47.284	1.00	14.10	5566	CB	PHE A 830	33.982	0.683	43.674	1.00	18.77
5514	O	ARG A 824	37.659	-1.363	46.894	1.00	15.81	5567	CD1	PHE A 830	33.498	1.663	42.823	1.00	17.67
5515	CB	ARG A 824	38.584	1.423	45.592	1.00	13.50	5568	CD2	PHE A 830	33.671	0.733	45.029	1.00	19.33
5516	CG	ARG A 824	38.612	0.463	44.411	1.00	12.90	5569	CE1	PHE A 830	32.667	2.668	43.352	1.00	18.46
5517	CD	ARG A 824	39.803	0.839	43.450	1.00	14.06	5570	CE2	PHE A 830	32.777	1.688	45.534	1.00	18.20
5518	NE	ARG A 824	39.853	-0.095	42.310	1.00	12.64	5571	CZ	PHE A 830	32.304	2.663	44.685	1.00	18.78
5519	CZ	ARG A 824	39.049	-0.024	41.238	1.00	14.31	5572	N	ARG A 831	35.349	-3.406	41.627	1.00	15.44
5520	NH1	ARG A 824	38.127	0.944	41.136	1.00	13.55	5573	CA	ARG A 831	36.378	-4.252	41.039	1.00	16.14
5521	NH2	ARG A 824	39.174	-0.928	40.254	1.00	14.66	5574	C	ARG A 831	35.894	-5.556	40.438	1.00	16.54
5522	N	ASN A 825	39.145	-0.268	48.232	1.00	14.31	5575	O	ARG A 831	36.425	-6.657	40.688	1.00	16.91
5523	CA	ASN A 825	39.689	-1.523	48.760	1.00	16.54	5576	CB	ARG A 831	37.362	-4.574	42.188	1.00	16.96
5524	C	ASN A 825	38.644	-2.390	49.496	1.00	15.73	5577	CG	ARG A 831	38.080	-3.419	42.858	1.00	16.46
5525	O	ASN A 825	38.693	-3.608	49.448	1.00	12.95	5578	CD	ARG A 831	38.971	-3.779	44.005	1.00	17.94
5526	CB	ASN A 825	40.877	-1.380	49.720	1.00	14.70	5579	NE	ARG A 831	38.365	-3.942	45.328	1.00	17.80
5527	CG	ASN A 825	42.129	-0.771	49.136	1.00	17.12	5580	CZ	ARG A 831	38.198	-5.082	45.971	1.00	18.41
5528	OD1	ASN A 825	42.988	-0.200	49.853	1.00	19.07	5581	NH1	ARG A 831	38.542	-6.244	45.421	1.00	18.63
5529	ND2	ASN A 825	42.310	-0.737	47.823	1.00	13.10	5582	NH2	ARG A 831	37.617	-5.115	47.169	1.00	18.47
5530	N	GLN A 826	37.741	-1.663	50.181	1.00	18.02	5583	N	MET A 832	34.819	-5.468	39.649	1.00	16.98
5531	CA	GLN A 826	36.695	-2.358	50.934	1.00	20.90	5584	CA	MET A 832	34.280	-6.623	38.923	1.00	16.56
5532	C	GLN A 826	35.477	-2.876	50.182	1.00	20.36	5585	C	MET A 832	35.367	-7.141	37.961	1.00	17.92
5533	O	GLN A 826	34.651	-3.630	50.742	1.00	19.69	5586	O	MET A 832	36.184	-6.323	37.488	1.00	17.69
5534	CB	GLN A 826	36.132	-1.381	51.993	1.00	26.32	5587	CB	MET A 832	33.002	-6.169	38.210	1.00	16.53
5535	CG	GLN A 826	36.580	-1.691	53.397	1.00	35.56	5588	CG	MET A 832	31.834	-5.953	39.241	1.00	15.93
5536	CD	GLN A 826	36.182	-3.094	53.844	1.00	39.06	5589	SD	MET A 832	30.273	-5.680	38.352	1.00	14.50
5537	OB1	GLN A 826	35.589	-3.891	53.119	1.00	42.26	5590	CE	MET A 832	30.215	-3.878	38.401	1.00	13.68
5538	NE2	GLN A 826	36.412	-3.345	55.128	1.00	41.91	5591	N	THR A 833	35.416	-8.440	37.714	1.00	16.30
5539	N	HIS A 827	35.234	-2.404	48.976	1.00	16.91	5592	CA	THR A 833	36.465	-8.992	36.872	1.00	17.66
5540	CA	HIS A 827	34.036	-2.689	48.202	1.00	16.78	5593	C	THR A 833	36.119	-9.364	35.440	1.00	19.22
5541	O	HIS A 827	34.350	-3.273	46.840	1.00	15.74	5594	O	THR A 833	37.057	-9.531	34.621	1.00	17.30
5542	C	HIS A 827	34.555	-2.536	45.872	1.00	13.89	5595	CB	THR A 833	37.064	-10.227	37.580	1.00	17.12
5543	CB	HIS A 827	33.257	-1.326	48.096	1.00	15.20	5596	OG1	THR A 833	36.053	-11.222	37.737	1.00	18.20
5544	CG	HIS A 827	32.617	-0.988	49.413	1.00	16.26	5597	CG2	THR A 833	37.634	-9.883	38.959	1.00	16.91
5545	ND1	HIS A 827	33.202	-0.101	50.300	1.00	20.12	5598	N	THR A 834	34.820	-9.464	35.089	1.00	17.86
5546	CD2	HIS A 827	31.489	-1.420	50.032	1.00	14.76	5599	CA	THR A 834	34.456	-9.796	33.723	1.00	19.46
5547	CE1	HIS A 827	32.440	0.011	51.389	1.00	16.71	5600	C	THR A 834	33.566	-8.753	33.065	1.00	18.40
5548	NE2	HIS A 827	31.427	-0.829	51.254	1.00	19.08	5601	O	THR A 834	32.831	-8.051	33.768	1.00	18.40
5549	N	PRO A 828	34.325	-4.608	46.724	1.00	15.11	5602	CB	THR A 834	33.710	-11.144	33.592	1.00	19.44
5550	CA	PRO A 828	34.560	-5.321	45.497	1.00	14.14	5603	OG1	THR A 834	32.393	-10.968	34.125	1.00	20.68
5551	O	PRO A 828	33.561	-5.010	44.393	1.00	15.45	5604	CG2	THR A 834	34.421	-12.276	34.309	1.00	19.43
5552	C	PRO A 828	33.881	-5.329	43.255	1.00	15.72	5605	N	ALA A 835	33.566	-8.699	31.732	1.00	19.48
5553	CB	PRO A 828	34.468	-6.783	45.898	1.00	16.09	5606	CA	ALA A 835	32.648	-7.803	31.033	1.00	20.00
5554	CG	PRO A 828	33.621	-6.815	47.163	1.00	14.98	5607	C	ALA A 835	31.193	-8.165	31.312	1.00	20.77
5555	CD	PRO A 828	34.044	-5.548	47.851	1.00	14.73	5608	O	ALA A 835	30.385	-7.248	31.410	1.00	22.50
5556	N	ALA A 829	32.423	-4.314	44.652	1.00	14.28	5609	CB	ALA A 835	32.842	-7.825	29.508	1.00	18.74
5557	CA	ALA A 829	31.572	-3.851	43.558	1.00	14.18	5610	N	ASP A 836	30.790	-9.421	31.421	1.00	22.07
5558	C	ALA A 829	32.312	-2.961	42.554	1.00	15.27	5611	CA	ASP A 836	29.447	-9.864	31.696	1.00	23.30
5559	O	ALA A 829	31.927	-2.910	41.374	1.00	14.49	5612	C	ASP A 836	28.969	-9.388	33.066	1.00	21.99

5613	O	ASP A 836	27.808	-9.041	33.223	1.00	22.47	CG	LEU A 842	28.122	0.412	36.099	1.00	16.16
5614	CB	ASP A 836	29.282	-11.410	31.664	1.00	25.61	CD1	LEU A 842	29.646	0.464	36.201	1.00	15.40
5615	CB	ASP A 836	29.189	-11.927	30.230	1.00	27.82	CD2	LEU A 842	27.670	1.171	34.847	1.00	16.66
5616	OD1	ASP A 836	29.351	-13.150	30.024	1.00	30.02	N	THR A 843	24.433	0.335	35.896	1.00	18.55
5617	OD2	ASP A 836	29.058	-11.147	29.276	1.00	26.35	CA	THR A 843	23.509	0.996	34.955	1.00	19.55
5618	N	GLN A 837	29.844	-9.310	34.063	1.00	21.84	C	THR A 843	23.799	2.485	35.083	1.00	18.14
5619	CA	GLN A 837	29.453	-8.854	35.377	1.00	20.02	O	THR A 843	23.954	2.940	36.217	1.00	18.37
5620	C	GLN A 837	29.051	-7.386	35.296	1.00	18.66	CB	THR A 843	21.997	0.715	35.324	1.00	21.75
5621	O	GLN A 837	28.053	-7.047	35.906	1.00	17.00	OG1	THR A 843	21.984	0.728	36.780	1.00	27.30
5622	CB	GLN A 837	30.603	-8.904	36.400	1.00	21.90	CG2	THR A 843	21.591	-0.733	35.145	1.00	20.25
5623	CG	GLN A 837	30.712	-10.131	37.263	1.00	22.49	N	PHE A 844	23.800	3.289	34.050	1.00	17.73
5624	CD	GLN A 837	31.790	-9.982	38.343	1.00	21.99	CA	PHE A 844	23.831	4.740	34.087	1.00	17.70
5625	OE1	GLN A 837	32.918	-9.616	38.024	1.00	20.17	C	PHE A 844	22.432	5.276	34.395	1.00	19.50
5626	NE2	GLN A 837	31.367	-10.297	39.564	1.00	20.64	O	PHE A 844	21.404	4.713	33.999	1.00	17.81
5627	N	ILE A 838	29.898	-6.608	34.623	1.00	16.54	CB	PHE A 844	24.393	5.290	32.769	1.00	19.16
5628	CA	ILE A 838	29.667	-5.167	34.499	1.00	18.19	CG	PHE A 844	25.890	4.994	32.659	1.00	18.93
5629	C	ILE A 838	28.370	-4.877	33.740	1.00	20.92	CD1	PHE A 844	26.336	3.998	31.778	1.00	19.58
5630	O	ILE A 838	27.578	-3.998	34.152	1.00	18.47	CD2	PHE A 844	26.805	5.688	33.423	1.00	17.53
5631	CB	ILE A 838	30.895	-4.516	33.835	1.00	19.11	CE1	PHE A 844	27.691	3.718	31.666	1.00	16.61
5632	CG1	ILE A 838	32.141	-4.578	34.778	1.00	16.48	CE2	PHE A 844	28.161	5.407	33.322	1.00	16.61
5633	CG2	ILE A 838	30.618	-3.062	33.428	1.00	18.17	CZ	PHE A 845	28.604	4.408	32.474	1.00	16.03
5634	CD1	ILE A 838	33.422	-4.259	33.992	1.00	16.81	N	LEU A 845	22.317	6.283	35.262	1.00	20.29
5635	N	LYS A 839	28.126	-5.604	32.642	1.00	20.40	CA	LEU A 845	21.038	6.840	35.660	1.00	21.27
5636	CA	LYS A 839	26.868	-5.425	31.895	1.00	24.05	C	LEU A 845	20.919	8.200	34.954	1.00	23.53
5637	C	LYS A 839	25.681	-5.781	32.770	1.00	25.13	O	LEU A 845	21.935	8.833	34.636	1.00	23.88
5638	O	LYS A 839	24.646	-5.116	32.756	1.00	26.96	CB	LEU A 845	20.935	7.051	37.170	1.00	21.66
5639	CB	LYS A 839	26.836	-6.328	30.636	1.00	24.14	CG	LEU A 845	21.162	5.826	38.092	1.00	23.12
5640	CG	LYS A 839	27.894	-5.833	29.641	1.00	26.39	CD1	LEU A 845	21.274	6.272	39.546	1.00	22.17
5641	CD	LYS A 839	27.580	-6.351	28.235	1.00	30.49	CD2	LEU A 845	20.052	4.791	37.920	1.00	23.11
5642	CE	LYS A 839	28.219	-7.705	28.025	1.00	32.93	N	GLU A 846	19.690	8.626	34.698	1.00	21.38
5643	NZ	LYS A 839	28.865	-7.658	26.661	1.00	35.80	CA	GLU A 846	19.490	9.929	34.070	1.00	24.30
5644	N	GLN A 840	25.788	-6.819	33.588	1.00	25.00	C	GLU A 846	19.991	11.035	34.975	1.00	21.71
5645	CA	GLN A 840	24.684	-7.184	34.471	1.00	26.52	O	GLU A 846	19.653	11.010	36.172	1.00	20.11
5646	C	GLN A 840	24.438	-6.235	35.642	1.00	24.27	CB	GLU A 846	17.975	10.166	33.842	1.00	28.61
5647	O	GLN A 840	23.285	-6.041	36.067	1.00	21.92	CG	GLU A 846	17.724	11.373	32.965	1.00	34.76
5648	CB	GLN A 840	25.070	-8.548	35.028	1.00	31.74	CD	GLU A 846	17.726	12.749	33.588	1.00	39.53
5649	CG	GLN A 840	23.972	-9.403	35.610	1.00	39.43	OE1	GLU A 846	18.229	13.687	32.884	1.00	41.56
5650	CD	GLN A 840	24.253	-10.889	35.404	1.00	43.34	OE2	GLU A 846	17.272	13.005	34.732	1.00	40.66
5651	OE1	GLN A 840	23.875	-11.733	36.232	1.00	45.14	N	SER A 847	20.680	12.026	34.430	1.00	19.82
5652	NE2	GLN A 840	24.920	-11.257	34.306	1.00	44.87	CA	SER A 847	21.208	13.081	35.319	1.00	18.64
5653	N	ASN A 841	25.494	-5.678	36.234	1.00	17.87	C	SER A 847	21.368	14.319	34.462	1.00	19.77
5654	CA	ASN A 841	25.352	-4.940	37.483	1.00	19.33	O	SER A 847	21.263	14.210	33.233	1.00	18.46
5655	C	ASN A 841	25.456	-3.442	37.474	1.00	17.58	CB	SER A 847	22.527	12.667	36.002	1.00	17.95
5656	O	ASN A 841	25.171	-2.831	38.520	1.00	17.51	OG	SER A 847	23.592	12.595	35.047	1.00	19.81
5657	CB	ASN A 841	26.468	-5.479	38.436	1.00	20.01	N	PRO A 848	21.622	15.466	35.068	1.00	20.84
5658	CG	ASN A 841	26.318	-6.928	38.823	1.00	21.30	CA	PRO A 848	21.738	16.711	34.326	1.00	21.84
5659	OD1	ASN A 841	27.336	-7.581	39.153	1.00	24.17	O	PRO A 848	23.896	16.064	33.439	1.00	22.58
5660	ND2	ASN A 841	25.136	-7.506	38.867	1.00	17.31	C	PRO A 848	21.911	17.756	35.428	1.00	21.32
5661	N	LEU A 842	25.969	-2.825	36.425	1.00	17.66	CB	PRO A 848	21.911	17.756	35.428	1.00	21.32
5662	CA	LEU A 842	26.184	-1.376	36.377	1.00	17.63	CG	PRO A 848	21.153	17.200	36.614	1.00	21.13
5663	C	LEU A 842	25.163	-0.724	35.461	1.00	18.99	CD	PRO A 848	21.503	15.705	36.538	1.00	20.99
5664	O	LEU A 842	25.011	-1.186	34.306	1.00	17.85	N	THR A 849	22.785	17.738	32.406	1.00	24.17
5665	CB	LEU A 842	27.657	-1.086	35.967	1.00	16.31	CA	THR A 849	23.849	17.972	31.424	1.00	24.95

5719	C	THR A 849	25.242	18.088	32.050	1.00	22.16	5772	CA	LEU A 856	26.188	-0.794	41.188	1.00	18.95
5720	O	THR A 849	25.493	18.737	33.071	1.00	21.14	5773	C	LEU A 856	25.172	-1.634	41.962	1.00	18.66
5721	CB	THR A 849	23.540	19.287	30.661	1.00	24.81	5774	O	LEU A 856	24.868	-1.303	43.156	1.00	20.65
5722	OG1	THR A 849	22.271	19.114	30.029	1.00	25.94	5775	CB	LEU A 856	27.582	-0.729	41.838	1.00	15.58
5723	CG2	THR A 849	24.626	19.557	29.609	1.00	25.93	5776	CG	LEU A 856	28.600	0.261	41.242	1.00	15.91
5724	N	ASN A 850	26.201	17.420	31.423	1.00	20.59	5777	CD1	LEU A 856	29.935	0.194	42.026	1.00	15.73
5725	CA	ASN A 850	27.600	17.432	31.834	1.00	20.77	5778	CD2	LEU A 856	28.851	-0.034	39.762	1.00	15.55
5726	C	ASN A 850	27.795	16.847	33.239	1.00	19.84	5779	N	LYS A 857	24.482	-2.559	41.308	1.00	20.01
5727	O	ASN A 850	28.665	17.266	34.020	1.00	18.02	5780	CA	LYS A 857	23.349	-3.244	41.916	1.00	21.47
5728	CB	ASN A 850	28.286	18.778	31.664	1.00	20.31	5781	C	LYS A 857	23.415	-4.614	42.559	1.00	19.85
5729	CG	ASN A 850	29.817	18.702	31.663	1.00	21.52	5782	O	LYS A 857	24.129	-5.512	42.141	1.00	16.38
5730	OD1	ASN A 850	30.384	17.768	31.100	1.00	19.79	5783	CB	LYS A 857	22.273	-3.433	40.784	1.00	23.29
5731	ND2	ASN A 850	30.504	19.668	32.261	1.00	18.52	5784	CG	LYS A 857	21.724	-2.106	40.284	1.00	26.57
5732	N	THR A 851	27.040	15.769	33.508	1.00	18.54	5785	CD	LYS A 857	20.895	-2.342	38.990	1.00	28.26
5733	CA	THR A 851	27.234	14.985	34.728	1.00	19.54	5786	CE	LYS A 857	21.874	-2.829	37.915	1.00	29.07
5734	C	THR A 851	26.541	13.150	33.375	1.00	18.01	5787	NZ	LYS A 857	21.301	-3.488	36.718	1.00	28.50
5735	O	THR A 851	26.235	15.237	35.873	1.00	18.24	5788	N	ASN A 858	22.551	-4.779	43.556	1.00	20.08
5736	CB	THR A 851	26.235	15.237	35.873	1.00	18.24	5789	CA	ASN A 858	22.342	-6.017	44.296	1.00	22.03
5737	OG1	THR A 851	24.907	14.853	35.442	1.00	20.28	5790	C	ASN A 858	23.574	-6.787	44.771	1.00	19.15
5738	CG2	THR A 851	26.248	16.692	36.320	1.00	18.83	5791	O	ASN A 858	23.832	-7.961	44.451	1.00	17.47
5739	N	VAL A 852	27.723	12.627	35.230	1.00	18.35	5792	CB	ASN A 858	21.481	-6.963	43.428	1.00	24.99
5740	CA	VAL A 852	27.673	11.190	34.978	1.00	18.50	5793	CG	ASN A 858	20.672	-7.932	44.294	1.00	27.08
5741	C	VAL A 852	27.277	10.516	36.296	1.00	19.16	5794	OD1	ASN A 858	20.308	-7.642	45.418	1.00	25.89
5742	O	VAL A 852	28.012	10.724	37.265	1.00	16.89	5795	ND2	ASN A 858	20.346	-9.104	43.726	1.00	28.26
5743	CB	VAL A 852	29.064	10.638	34.571	1.00	20.21	5796	N	TYR A 859	24.290	-6.198	45.719	1.00	15.00
5744	CG1	VAL A 852	29.058	9.112	34.604	1.00	18.62	5797	CA	TYR A 859	25.524	-6.732	46.272	1.00	15.84
5745	CG2	VAL A 852	29.530	11.124	33.192	1.00	17.86	5798	C	TYR A 859	26.470	-7.231	45.162	1.00	14.81
5746	N	ALA A 853	26.272	9.662	36.315	1.00	17.66	5799	O	TYR A 859	26.871	-8.386	45.149	1.00	13.23
5747	CA	ALA A 853	25.839	8.989	37.544	1.00	16.64	5800	CB	TYR A 859	25.147	-7.865	47.215	1.00	17.53
5748	C	ALA A 853	25.511	7.540	37.210	1.00	17.67	5801	CD1	TYR A 859	24.243	-7.457	48.362	1.00	18.89
5749	O	ALA A 853	24.951	7.276	36.117	1.00	18.63	5802	CG1	TYR A 859	22.870	-7.641	48.244	1.00	20.51
5750	CB	ALA A 853	24.565	9.709	38.039	1.00	15.15	5803	CD2	TYR A 859	24.719	-6.915	49.548	1.00	17.97
5751	N	PHE A 854	25.863	6.606	38.068	1.00	16.51	5804	CE1	TYR A 859	21.995	-7.319	49.262	1.00	20.07
5752	CA	PHE A 854	25.701	5.180	37.832	1.00	17.75	5805	CE2	TYR A 859	23.860	-6.602	50.574	1.00	18.09
5753	C	PHE A 854	25.400	4.431	39.126	1.00	18.33	5806	CZ	TYR A 859	22.496	-6.786	50.428	1.00	21.56
5754	O	PHE A 854	25.573	4.950	40.251	1.00	19.36	5807	OH	TYR A 859	21.657	-6.473	51.472	1.00	20.57
5755	CB	PHE A 854	26.922	4.577	37.103	1.00	18.03	5808	N	ALA A 860	26.756	-6.405	44.195	1.00	14.63
5756	CG	PHE A 854	28.266	4.665	37.791	1.00	18.64	5809	CA	ALA A 860	27.573	-6.753	43.030	1.00	16.97
5757	CD1	PHE A 854	28.705	3.655	38.635	1.00	19.06	5810	C	ALA A 860	28.955	-7.249	43.442	1.00	18.77
5758	CD2	PHE A 854	29.117	5.734	37.569	1.00	18.31	5811	O	ALA A 860	29.597	-6.651	44.336	1.00	19.26
5759	CE1	PHE A 854	29.952	3.745	39.251	1.00	17.32	5812	CB	ALA A 860	27.744	-5.511	42.164	1.00	18.48
5760	CE2	PHE A 854	30.366	5.799	38.148	1.00	17.33	5813	N	ASN A 861	29.362	-8.365	42.860	1.00	18.35
5761	CZ	PHE A 854	30.793	4.792	39.003	1.00	15.66	5814	CA	ASN A 861	30.655	-8.995	43.164	1.00	18.84
5762	N	GLU A 855	24.837	3.226	38.985	1.00	18.41	5815	C	ASN A 861	30.855	-9.139	44.672	1.00	19.08
5763	CA	GLU A 855	24.385	2.432	40.134	1.00	17.60	5816	O	ASN A 861	31.935	-8.866	45.226	1.00	18.01
5764	C	GLU A 855	24.952	1.008	40.033	1.00	17.60	5817	CB	ASN A 861	31.796	-8.205	42.485	1.00	18.52
5765	O	GLU A 855	25.011	0.485	38.900	1.00	15.72	5818	CG	ASN A 861	33.144	-8.920	42.430	1.00	18.65
5766	CB	GLU A 855	22.839	2.373	40.213	1.00	17.57	5819	OD1	ASN A 861	33.182	-10.129	42.202	1.00	18.09
5767	CG	GLU A 855	22.296	1.628	41.437	1.00	18.25	5820	ND2	ASN A 861	34.255	-8.206	42.638	1.00	16.42
5768	CD	GLU A 855	20.756	1.617	41.583	1.00	21.29	5821	N	HIS A 862	29.923	-9.745	45.420	1.00	18.36
5769	OE1	GLU A 855	20.194	1.168	42.603	1.00	22.85	5822	CA	HIS A 862	29.912	-10.026	46.835	1.00	18.01
5770	OE2	GLU A 855	20.095	2.079	40.611	1.00	22.94	5823	C	HIS A 862	30.326	-8.786	47.655	1.00	18.23
5771	N	LEU A 856	25.606	0.580	41.096	1.00	17.21	5824	O	HIS A 862	31.071	-8.845	48.634	1.00	19.16

5825	CB	HIS A 862	30.725	-11.267	47.307	1.00	18.46	5878	CA	ILE A 868	25.644	1.902	45.360	1.00	17.77
5826	CG	HIS A 862	32.194	-11.226	46.999	1.00	20.04	5879	C	ILE A 868	25.425	2.872	44.217	1.00	17.69
5827	ND1	HIS A 862	32.690	-11.802	45.836	1.00	21.25	5880	O	ILE A 868	25.330	2.391	43.094	1.00	18.10
5828	CD2	HIS A 862	33.279	-10.659	47.560	1.00	21.51	5881	CB	ILE A 868	27.127	1.424	45.318	1.00	18.75
5829	CE1	HIS A 862	33.983	-11.616	45.725	1.00	21.85	5882	CG1	ILE A 868	27.433	0.426	46.467	1.00	19.10
5830	NE2	HIS A 862	34.380	-10.896	46.767	1.00	23.07	5883	CG2	ILE A 868	28.041	2.639	45.602	1.00	18.17
5831	N	ASP A 863	29.770	-7.637	47.354	1.00	16.12	5884	CD1	ILE A 868	28.866	-0.183	46.382	1.00	19.08
5832	CA	ASP A 863	29.883	-6.424	48.130	1.00	17.57	5885	N	ILE A 869	25.397	4.154	44.510	1.00	16.22
5833	C	ASP A 863	28.980	-6.498	49.361	1.00	16.17	5886	CA	ILE A 869	25.256	5.150	43.447	1.00	15.16
5834	O	ASP A 863	27.999	-7.241	49.361	1.00	15.89	5887	C	ILE A 869	26.496	6.039	43.528	1.00	15.96
5835	CB	ASP A 863	29.435	-5.250	47.242	1.00	17.41	5888	O	ILE A 869	26.936	6.380	44.637	1.00	17.68
5836	CG	ASP A 863	30.045	-3.935	47.687	1.00	19.24	5889	CB	ILE A 869	23.932	5.949	43.590	1.00	14.79
5837	OD1	ASP A 863	31.158	-3.597	47.207	1.00	15.53	5890	CG1	ILE A 869	22.753	5.177	43.024	1.00	16.18
5838	OD2	ASP A 863	29.459	-3.191	48.509	1.00	20.34	5891	CG2	ILE A 869	24.060	7.342	42.951	1.00	14.77
5839	N	THR A 864	29.270	-5.700	50.388	1.00	16.93	5892	CD1	ILE A 869	21.309	5.688	43.251	1.00	17.74
5840	CA	THR A 864	28.442	-5.615	51.570	1.00	17.66	5893	N	VAL A 870	27.084	6.345	42.385	1.00	13.11
5841	C	THR A 864	27.315	-4.585	51.445	1.00	19.37	5894	CA	VAL A 870	28.208	7.276	42.308	1.00	15.88
5842	O	THR A 864	26.382	-4.558	52.256	1.00	19.59	5895	C	VAL A 870	27.777	8.403	41.357	1.00	13.78
5843	CB	THR A 864	29.230	-5.242	52.846	1.00	18.03	5896	O	VAL A 870	27.303	8.071	40.277	1.00	14.36
5844	CG1	THR A 864	30.031	-4.081	52.545	1.00	18.52	5897	CB	VAL A 870	29.500	6.597	41.787	1.00	16.19
5845	CG2	THR A 864	30.062	-6.428	53.337	1.00	17.90	5898	CG1	VAL A 870	30.634	7.584	41.464	1.00	17.02
5846	N	TRP A 865	27.378	-3.754	50.419	1.00	18.22	5899	CG2	VAL A 870	29.989	5.575	42.845	1.00	15.31
5847	CA	TRP A 865	26.366	-2.703	50.191	1.00	19.88	5900	N	MET A 871	28.093	9.657	41.556	1.00	15.32
5848	C	TRP A 865	25.478	-3.241	49.072	1.00	21.10	5901	CA	MET A 871	27.849	10.659	40.508	1.00	16.32
5849	O	TRP A 865	25.965	-3.703	48.039	1.00	19.83	5902	C	MET A 871	28.985	11.671	40.520	1.00	16.77
5850	CB	TRP A 865	27.055	-1.385	49.870	1.00	20.11	5903	O	MET A 871	29.341	12.115	41.624	1.00	16.61
5851	CG	TRP A 865	27.697	-0.603	50.975	1.00	20.00	5904	CB	MET A 871	26.511	11.402	40.645	1.00	17.18
5852	CD1	TRP A 865	27.512	-0.899	52.310	1.00	20.46	5905	CG	MET A 871	26.303	12.711	39.875	1.00	18.06
5853	CD2	TRP A 865	28.490	0.608	50.952	1.00	19.16	5906	SD	MET A 871	24.576	13.307	40.042	1.00	17.89
5854	NE1	TRP A 865	28.207	-0.016	53.072	1.00	19.59	5907	CE	MET A 871	24.717	14.958	39.345	1.00	17.65
5855	CE2	TRP A 865	28.808	0.918	52.281	1.00	20.04	5908	N	TYR A 872	29.496	11.964	39.333	1.00	15.67
5856	CE3	TRP A 865	29.016	1.392	49.936	1.00	18.40	5909	CA	TYR A 872	30.520	13.001	39.181	1.00	17.64
5857	CZ2	TRP A 865	29.584	2.019	52.639	1.00	19.58	5910	C	TYR A 872	29.866	14.313	38.765	1.00	17.57
5858	CZ3	TRP A 865	29.777	2.502	50.287	1.00	20.06	5911	O	TYR A 872	29.125	14.271	37.786	1.00	18.01
5859	CH2	TRP A 865	30.082	2.782	51.624	1.00	18.82	5912	CB	TYR A 872	31.569	12.699	38.081	1.00	16.70
5860	N	LYS A 866	24.171	-3.257	49.278	1.00	18.45	5913	CG	TYR A 872	32.156	11.318	38.208	1.00	16.28
5861	CA	LYS A 866	23.184	-3.732	48.319	1.00	20.04	5914	CD1	TYR A 872	32.120	10.472	37.110	1.00	13.82
5862	C	LYS A 866	23.133	-2.967	47.004	1.00	19.12	5915	CD2	TYR A 872	32.651	10.833	39.432	1.00	17.04
5863	O	LYS A 866	23.316	-3.533	45.926	1.00	16.36	5916	CE1	TYR A 872	32.631	9.180	37.193	1.00	15.56
5864	CB	LYS A 866	21.813	-3.689	49.002	1.00	20.69	5917	CE2	TYR A 872	33.138	9.522	39.527	1.00	16.23
5865	CG	LYS A 866	20.635	-4.165	48.181	1.00	25.35	5918	CZ	TYR A 872	33.069	8.696	38.405	1.00	16.02
5866	CD	LYS A 866	19.462	-4.533	49.094	1.00	30.56	5919	OH	TYR A 872	33.528	7.402	38.433	1.00	16.10
5867	CE	LYS A 866	18.162	-4.133	48.385	1.00	32.55	5920	N	ASN A 873	30.114	15.425	39.416	1.00	18.25
5868	NZ	LYS A 866	17.703	-5.263	47.516	1.00	36.93	5921	CA	ASN A 873	29.599	16.720	39.021	1.00	17.41
5869	N	ASN A 867	22.957	-1.640	47.085	1.00	17.81	5922	C	ASN A 873	30.804	17.644	38.874	1.00	17.53
5870	CA	ASN A 867	22.992	-0.817	45.878	1.00	19.57	5923	O	ASN A 873	31.181	18.240	39.867	1.00	18.67
5871	C	ASN A 867	23.954	0.339	46.119	1.00	19.05	5924	CB	ASN A 873	28.650	17.362	40.055	1.00	18.79
5872	O	ASN A 867	23.947	0.830	47.255	1.00	17.99	5925	CG	ASN A 873	28.169	18.759	39.681	1.00	19.71
5873	CB	ASN A 867	21.656	-0.244	45.428	1.00	19.15	5926	OD1	ASN A 873	28.219	19.179	38.513	1.00	19.99
5874	CG1	ASN A 867	20.650	-1.322	45.045	1.00	20.68	5927	ND2	ASN A 873	27.768	19.612	40.630	1.00	16.40
5875	OD1	ASN A 867	20.987	-2.249	44.295	1.00	20.32	5928	N	PRO A 874	31.324	17.850	37.673	1.00	17.92
5876	ND2	ASN A 867	19.422	-1.255	45.549	1.00	17.97	5929	CA	PRO A 874	32.426	18.758	37.448	1.00	18.85
5877	N	ILE A 868	24.751	0.805	45.213	1.00	18.06	5930	C	PRO A 874	31.964	20.201	37.260	1.00	20.43

5931	O	PRO A 874	32.857	21.062	37.114	1.00	19.83	5984	O	LEU A 881	18.363	13.335	42.617	1.00	17.14
5932	CB	PRO A 874	33.028	18.250	36.120	1.00	18.54	5985	CB	LEU A 881	21.058	12.982	41.365	1.00	18.29
5933	CG	PRO A 874	31.814	17.776	35.350	1.00	18.34	5986	CG	LEU A 881	21.001	11.492	41.039	1.00	20.54
5934	CD	PRO A 874	30.927	17.154	36.432	1.00	18.38	5987	CD1	LEU A 881	21.214	11.306	39.528	1.00	21.58
5935	N	ASN A 875	30.658	20.487	37.266	1.00	18.81	5988	CD2	LEU A 881	22.087	10.699	41.817	1.00	20.54
5936	CA	ASN A 875	30.197	21.862	37.056	1.00	21.71	5989	N	ASN A 882	17.745	12.668	40.578	1.00	18.74
5937	C	ASN A 875	30.401	22.836	38.198	1.00	21.33	5990	CA	ASN A 882	16.529	11.983	40.974	1.00	20.32
5938	O	ASN A 875	30.422	22.397	39.369	1.00	20.55	5991	C	ASN A 882	16.916	10.547	41.262	1.00	19.51
5939	CB	ASN A 875	28.687	21.786	36.701	1.00	22.52	5992	O	ASN A 882	17.686	9.944	40.505	1.00	21.26
5940	CG	ASN A 875	28.451	20.853	35.519	1.00	24.12	5993	CB	ASN A 882	15.547	12.040	39.832	1.00	24.52
5941	OD1	ASN A 875	28.894	21.182	34.417	1.00	26.00	5994	CG	ASN A 882	15.024	13.451	39.705	1.00	27.48
5942	ND2	ASN A 875	27.799	19.711	35.664	1.00	21.36	5995	OD1	ASN A 882	14.600	14.087	40.666	1.00	28.76
5943	N	LYS A 876	30.486	24.146	37.974	1.00	21.86	5996	ND2	ASN A 882	15.063	13.946	38.456	1.00	20.00
5944	CA	LYS A 876	30.645	25.159	39.028	1.00	25.54	5997	N	LEU A 883	16.404	9.998	42.341	1.00	20.69
5945	C	LYS A 876	29.380	25.447	39.861	1.00	23.68	5998	CA	LEU A 883	16.795	8.686	42.799	1.00	19.88
5946	O	LYS A 876	29.408	26.291	40.768	1.00	20.96	5999	C	LEU A 883	15.763	7.565	42.619	1.00	21.80
5947	CB	LYS A 876	31.049	26.536	38.435	1.00	28.74	6000	O	LEU A 883	14.583	7.773	42.723	1.00	23.04
5948	CG	LYS A 876	32.446	26.518	37.768	1.00	32.96	6001	CB	LEU A 883	17.076	8.771	44.330	1.00	19.20
5949	CD	LYS A 876	33.382	26.138	38.926	1.00	35.88	6002	CG	LEU A 883	18.161	9.773	44.743	1.00	19.84
5950	CE	LYS A 876	34.570	27.098	39.033	1.00	37.37	6003	CD1	LEU A 883	18.166	10.045	46.259	1.00	20.56
5951	NZ	LYS A 876	35.469	26.778	37.875	1.00	36.83	6004	CD2	LEU A 883	19.510	9.241	44.291	1.00	15.99
5952	N	THR A 877	28.261	24.779	39.591	1.00	22.70	6005	N	PRO A 884	16.303	6.364	42.482	1.00	20.55
5953	CA	THR A 877	27.057	24.946	40.425	1.00	22.49	6006	CA	PRO A 884	15.498	5.168	42.474	1.00	23.11
5954	C	THR A 877	26.579	23.547	40.821	1.00	21.81	6007	C	PRO A 884	14.757	5.106	43.809	1.00	22.93
5955	O	THR A 877	26.865	22.555	40.163	1.00	19.74	6008	O	PRO A 884	15.119	5.780	44.796	1.00	21.23
5956	CB	THR A 877	25.891	22.589	39.673	1.00	22.36	6009	CB	PRO A 884	16.530	4.053	42.301	1.00	22.91
5957	CG1	THR A 877	25.632	24.830	38.499	1.00	23.54	6010	CG	PRO A 884	17.714	4.713	41.660	1.00	21.54
5958	CG2	THR A 877	26.212	27.030	39.271	1.00	25.23	6011	CD	PRO A 884	17.762	6.046	42.397	1.00	20.96
5959	N	THR A 878	25.857	23.541	41.955	1.00	18.08	6012	N	SER A 885	13.760	4.240	43.934	1.00	21.66
5960	CA	SER A 878	25.326	22.269	42.406	1.00	18.86	6013	CA	SER A 885	12.967	4.273	45.162	1.00	24.40
5961	C	SER A 878	24.284	21.737	41.420	1.00	19.86	6014	C	SER A 885	13.716	3.881	46.431	1.00	23.95
5962	O	SER A 878	23.661	22.481	40.673	1.00	18.20	6015	O	SER A 885	14.814	3.285	46.467	1.00	21.34
5963	CB	SER A 878	24.366	22.598	43.617	1.00	16.87	6016	CB	SER A 885	11.706	3.395	44.996	1.00	25.34
5964	CG	SER A 878	23.469	23.709	43.603	1.00	20.00	6017	OG	SER A 885	12.206	2.088	45.063	1.00	26.34
5965	N	GLN A 879	24.144	20.400	41.475	1.00	20.32	6018	N	GLY A 886	13.117	4.365	47.544	1.00	21.95
5966	CA	GLN A 879	23.180	19.790	40.580	1.00	21.86	6019	CA	GLY A 886	13.647	3.960	48.850	1.00	21.89
5967	C	GLN A 879	22.200	18.733	41.224	1.00	22.97	6020	C	GLY A 886	14.483	4.998	49.573	1.00	22.67
5968	O	GLN A 879	22.675	18.029	42.131	1.00	21.65	6021	O	GLY A 886	14.689	6.146	49.165	1.00	23.42
5969	CB	GLN A 879	23.931	18.974	39.468	1.00	22.37	6022	N	ASP A 887	14.869	4.680	50.801	1.00	21.05
5970	CG	GLN A 879	24.910	19.802	38.645	1.00	22.60	6023	CA	ASP A 887	15.760	5.451	51.645	1.00	22.50
5971	CD	GLN A 879	24.240	20.815	37.750	1.00	23.49	6024	C	ASP A 887	17.214	5.281	51.210	1.00	20.68
5972	OE1	GLN A 879	23.305	20.445	37.029	1.00	24.49	6025	O	ASP A 887	17.634	4.130	51.040	1.00	19.39
5973	NE2	GLN A 879	24.740	22.035	37.686	1.00	23.81	6026	CB	ASP A 887	15.602	4.969	53.086	1.00	23.02
5974	N	THR A 880	20.980	18.539	40.721	1.00	20.70	6027	CG	ASP A 887	16.484	5.799	54.001	1.00	25.67
5975	CA	THR A 880	20.040	17.652	41.394	1.00	21.62	6028	OD1	ASP A 887	17.638	5.419	54.199	1.00	28.60
5976	C	THR A 880	19.919	16.302	40.713	1.00	18.77	6029	OD2	ASP A 887	16.009	6.815	54.502	1.00	20.00
5977	O	THR A 880	19.923	16.258	39.513	1.00	18.27	6030	N	TRP A 888	17.977	6.376	51.081	1.00	19.72
5978	CB	THR A 880	18.613	18.275	41.489	1.00	25.07	6031	CA	TRP A 888	19.375	6.298	50.691	1.00	17.29
5979	CG1	THR A 880	18.717	19.445	42.338	1.00	27.52	6032	C	TRP A 888	20.292	6.887	51.745	1.00	18.92
5980	CG2	THR A 880	17.672	17.294	42.200	1.00	26.46	6033	O	TRP A 888	19.985	7.977	52.265	1.00	19.35
5981	N	LEU A 881	20.041	15.196	41.424	1.00	17.50	6034	CB	TRP A 888	19.584	6.970	49.305	1.00	19.14
5982	CA	LEU A 881	19.883	13.866	40.872	1.00	17.31	6035	CG	TRP A 888	19.041	6.188	48.135	1.00	21.37
5983	C	LEU A 881	18.575	13.262	41.401	1.00	17.89	6036	CD1	TRP A 888	17.777	6.307	47.614	1.00	19.94



6037	CD2 TRP A 888	19.692	5.196	47.325	1.00	21.02	6090	N	GLN A 896	34.086	14.968	51.966	1.00	22.81
6038	NE1 TRP A 888	17.616	5.449	46.549	1.00	20.33	6091	CA	GLN A 896	33.930	13.925	52.976	1.00	22.65
6039	CE2 TRP A 888	18.775	4.742	46.365	1.00	21.10	6092	C	GLN A 896	33.662	12.612	52.237	1.00	22.28
6040	CE3 TRP A 888	20.966	4.626	47.345	1.00	23.66	6093	O	GLN A 896	32.744	12.496	51.436	1.00	19.57
6041	CZ2 TRP A 888	19.060	3.727	45.435	1.00	20.78	6094	CB	GLN A 896	32.781	14.173	53.958	1.00	24.18
6042	CZ3 TRP A 888	21.271	3.645	46.396	1.00	23.95	6095	CG	GLN A 896	32.835	15.288	54.933	1.00	28.13
6043	CH2 TRP A 888	20.330	3.181	45.469	1.00	21.41	6096	CD	GLN A 896	32.024	15.444	56.200	1.00	30.70
6044	N THR A 889	21.444	6.290	52.074	1.00	16.86	6097	OE1	GLN A 896	32.333	15.046	57.385	1.00	31.20
6045	CA THR A 889	22.397	6.862	53.008	1.00	17.70	6098	NE2	GLN A 896	30.906	16.146	56.043	1.00	23.23
6046	C THR A 889	23.506	7.623	52.293	1.00	18.48	6099	N	ILE A 897	34.546	11.646	52.545	1.00	20.05
6047	O THR A 889	24.068	7.059	51.330	1.00	17.19	6100	CA	ILE A 897	34.366	10.348	51.925	1.00	19.25
6048	CB THR A 889	23.071	5.754	53.870	1.00	18.89	6101	C	ILE A 897	34.674	9.206	53.003	1.00	17.61
6049	OG1 THR A 889	22.031	5.014	54.495	1.00	19.06	6102	O	ILE A 897	35.565	9.391	53.822	1.00	17.24
6050	CG2 THR A 889	23.995	6.360	54.928	1.00	16.36	6103	CB	ILE A 897	35.364	9.778	50.777	1.00	21.18
6051	N ILE A 890	23.827	8.864	52.643	1.00	17.13	6104	CG1	ILE A 897	35.494	11.058	49.949	1.00	19.62
6052	CA ILE A 890	24.908	9.575	51.956	1.00	18.82	6105	CG2	ILE A 897	34.751	8.692	49.874	1.00	24.68
6053	C ILE A 890	26.259	9.160	52.591	1.00	18.09	6106	CD1	ILE A 897	34.203	10.877	49.148	1.00	20.00
6054	O ILE A 890	26.349	9.198	53.816	1.00	18.88	6107	N	GLY A 898	33.824	8.166	53.012	1.00	18.75
6055	CB ILE A 890	24.732	11.089	52.093	1.00	18.96	6108	CA	GLY A 898	34.047	7.122	53.993	1.00	19.72
6056	CG1 ILE A 890	23.367	11.573	51.535	1.00	19.44	6109	C	GLY A 898	32.917	6.112	54.045	1.00	21.21
6057	CG2 ILE A 890	25.920	11.771	51.420	1.00	15.34	6110	O	GLY A 898	32.131	6.024	53.098	1.00	22.52
6058	CD1 ILE A 890	23.069	12.988	52.057	1.00	19.01	6111	N	GLU A 899	32.839	5.374	55.134	1.00	22.66
6059	N VAL A 891	27.241	8.700	51.844	1.00	17.95	6112	CA	GLU A 899	31.848	4.331	55.295	1.00	24.68
6060	CA VAL A 891	28.536	8.307	52.362	1.00	17.49	6113	C	GLU A 899	30.672	4.756	56.173	1.00	25.01
6061	C VAL A 891	29.719	9.089	51.748	1.00	17.57	6114	O	GLU A 899	29.690	4.011	56.229	1.00	25.22
6062	O VAL A 891	30.808	9.192	52.354	1.00	16.92	6115	CB	GLU A 899	32.539	3.087	55.883	1.00	25.95
6063	CB VAL A 891	28.904	6.821	52.307	1.00	18.15	6116	CG	GLU A 899	33.810	2.569	55.207	1.00	25.09
6064	CG1 VAL A 891	27.983	6.048	53.233	1.00	19.10	6117	CD	GLU A 899	33.525	1.712	53.981	1.00	25.77
6065	CG2 VAL A 891	28.997	6.205	50.921	1.00	18.18	6118	OE1	GLU A 899	32.401	1.155	53.967	1.00	25.14
6066	N GLY A 892	29.413	9.810	50.684	1.00	14.68	6119	OE2	GLU A 899	34.413	1.517	53.062	1.00	24.44
6067	CA GLY A 892	30.419	10.659	50.046	1.00	15.77	6120	N	LYS A 900	30.700	5.917	56.818	1.00	26.68
6068	C GLY A 892	29.792	12.007	49.641	1.00	18.34	6121	CA	LYS A 900	29.588	6.315	57.712	1.00	27.25
6069	O GLY A 892	28.876	11.911	48.821	1.00	15.50	6122	C	LYS A 900	28.562	7.272	57.137	1.00	25.12
6070	N LEU A 893	30.225	13.102	50.237	1.00	17.98	6123	O	LYS A 900	28.877	8.021	56.214	1.00	24.34
6071	CA LEU A 893	29.668	14.397	49.870	1.00	18.16	6124	CB	LYS A 900	30.138	6.954	58.991	1.00	30.47
6072	C LEU A 893	30.721	15.469	50.156	1.00	18.84	6125	CG	LYS A 900	31.166	8.056	58.815	1.00	34.16
6073	O LEU A 893	31.329	15.577	51.225	1.00	18.84	6126	CD	LYS A 900	31.252	8.901	60.073	1.00	37.55
6074	CB LEU A 893	28.353	14.725	50.598	1.00	18.93	6127	CE	LYS A 900	32.148	10.117	60.043	1.00	39.40
6075	CG LEU A 893	27.657	16.052	50.223	1.00	20.31	6128	NZ	LYS A 900	31.814	11.176	59.022	1.00	39.28
6076	CD1 LEU A 893	26.160	15.915	50.545	1.00	19.83	6129	N	SER A 901	27.347	7.305	57.686	1.00	22.18
6077	CD2 LEU A 893	28.199	17.314	50.895	1.00	19.07	6130	CA	SER A 901	26.272	8.150	57.221	1.00	19.86
6078	N GLY A 894	30.863	16.384	49.199	1.00	18.44	6131	C	SER A 901	26.602	9.636	57.424	1.00	20.90
6079	CA GLY A 894	31.780	17.536	49.376	1.00	19.33	6132	O	SER A 901	26.916	10.105	58.520	1.00	17.48
6080	C GLY A 894	33.173	16.936	49.592	1.00	21.53	6133	CB	SER A 901	24.943	7.837	57.959	1.00	20.68
6081	O GLY A 894	33.534	16.015	48.857	1.00	20.54	6134	OG	SER A 901	23.889	8.727	57.561	1.00	20.53
6082	N ASP A 895	33.906	17.393	50.605	1.00	20.89	6135	N	LEU A 902	26.313	10.398	56.397	1.00	20.11
6083	CA ASP A 895	35.240	16.835	50.842	1.00	22.34	6136	CA	LEU A 902	26.356	11.850	56.363	1.00	21.86
6084	C ASP A 895	35.191	15.680	51.834	1.00	22.18	6137	C	LEU A 902	24.905	12.352	56.257	1.00	21.44
6085	O ASP A 895	36.127	15.514	52.615	1.00	24.94	6138	O	LEU A 902	24.619	13.483	55.884	1.00	23.50
6086	CB ASP A 895	36.130	17.947	51.393	1.00	22.12	6139	CB	LEU A 902	27.161	12.292	55.123	1.00	20.45
6087	CG ASP A 895	35.478	18.553	52.622	1.00	23.64	6140	CB	LEU A 902	28.648	11.907	55.124	1.00	21.85
6088	OD1 ASP A 895	36.022	19.522	53.153	1.00	25.64	6141	CD1	LEU A 902	29.313	12.215	53.787	1.00	21.36
6089	OD2 ASP A 895	34.435	18.052	53.033	1.00	20.00	6142	CD2	LEU A 902	29.429	12.647	56.213	1.00	23.54

6143	N	GLY A 903	23.941	11.490	56.527	1.00	22.23	6196	CG	GLN A 910	19.856	19.985	46.266	1.00	27.05
6144	CA	GLY A 903	22.507	11.805	56.400	1.00	21.35	6197	CD	GLN A 910	19.701	21.417	46.720	1.00	30.96
6145	C	GLY A 903	21.755	10.820	55.503	1.00	22.85	6198	OE1	GLN A 910	20.065	22.155	45.819	1.00	34.28
6146	O	GLY A 903	22.304	9.974	54.773	1.00	21.12	6199	NE2	GLN A 910	19.496	21.840	47.984	1.00	20.00
6147	N	HIS A 904	20.416	10.897	55.544	1.00	21.69	6200	N	VAL A 911	23.796	17.686	44.736	1.00	19.28
6148	CA	HIS A 904	19.535	10.011	54.797	1.00	23.46	6201	CA	VAL A 911	25.245	17.405	44.720	1.00	17.62
6149	C	HIS A 904	18.628	10.789	53.870	1.00	23.10	6202	C	VAL A 911	26.083	18.669	44.564	1.00	16.72
6150	O	HIS A 904	18.198	11.869	54.301	1.00	24.57	6203	O	VAL A 911	25.929	19.417	43.604	1.00	15.75
6151	CB	HIS A 904	18.698	9.166	55.765	1.00	24.48	6204	CB	VAL A 911	25.574	16.486	43.522	1.00	18.06
6152	CG	HIS A 904	19.422	8.024	56.402	1.00	25.51	6205	CG1	VAL A 911	27.073	16.218	43.441	1.00	17.92
6153	ND1	HIS A 904	20.109	8.146	57.599	1.00	26.84	6206	CG2	VAL A 911	24.732	15.197	43.636	1.00	17.78
6154	CD2	HIS A 904	19.509	6.720	56.060	1.00	25.70	6207	N	PRO A 912	27.026	18.916	45.461	1.00	16.38
6155	CE1	HIS A 904	20.654	6.968	57.906	1.00	24.89	6208	CA	PRO A 912	27.871	20.082	45.470	1.00	17.42
6156	NE2	HIS A 904	20.287	6.092	57.025	1.00	20.66	6209	C	PRO A 912	28.675	20.351	44.198	1.00	18.48
6157	N	VAL A 905	18.379	10.385	52.631	1.00	20.66	6210	O	PRO A 912	29.107	19.443	43.466	1.00	16.06
6158	CA	VAL A 905	17.530	11.105	51.710	1.00	21.55	6211	CB	PRO A 912	28.858	19.807	46.625	1.00	18.95
6159	C	VAL A 905	16.686	10.142	50.856	1.00	22.40	6212	CG	PRO A 912	28.014	19.010	47.577	1.00	18.32
6160	O	VAL A 905	16.926	8.935	50.724	1.00	21.14	6213	CD	PRO A 912	27.262	18.053	46.667	1.00	17.58
6161	CB	VAL A 905	18.271	12.035	50.716	1.00	22.34	6214	N	ALA A 913	28.947	21.637	43.934	1.00	18.47
6162	CG1	VAL A 905	19.182	13.071	51.320	1.00	22.74	6215	CA	ALA A 913	29.792	21.934	42.767	1.00	18.97
6163	CG2	VAL A 905	19.108	11.151	49.778	1.00	22.37	6216	C	ALA A 913	31.156	21.235	42.809	1.00	19.12
6164	N	MET A 906	15.637	10.699	50.260	1.00	21.77	6217	O	ALA A 913	31.887	21.154	43.805	1.00	18.44
6165	CA	MET A 906	14.755	9.959	49.363	1.00	24.07	6218	CB	ALA A 913	30.037	23.434	42.685	1.00	19.77
6166	C	MET A 906	14.160	10.924	48.328	1.00	23.61	6219	N	ILE A 914	31.633	20.856	41.633	1.00	18.72
6167	O	MET A 906	14.031	12.130	48.524	1.00	22.79	6220	CA	ILE A 914	32.920	20.212	41.447	1.00	19.25
6168	CB	MET A 906	13.578	9.416	50.195	1.00	26.81	6221	C	ILE A 914	33.188	19.086	42.437	1.00	17.77
6169	CG	MET A 906	12.397	10.208	50.760	1.00	32.84	6222	O	ILE A 914	34.174	19.116	43.194	1.00	14.80
6170	SD	MET A 906	11.387	9.012	51.643	1.00	20.00	6223	CB	ILE A 914	34.148	21.132	41.309	1.00	23.32
6171	CE	MET A 906	11.948	7.311	51.468	1.00	20.00	6224	CG1	ILE A 914	34.131	22.434	40.505	1.00	20.00
6172	N	GLY A 907	13.907	10.353	47.148	1.00	21.83	6225	CG2	ILE A 914	35.175	20.189	40.657	1.00	20.00
6173	CA	GLY A 907	13.278	11.077	46.048	1.00	21.53	6226	CD1	ILE A 914	35.357	23.346	40.425	1.00	27.60
6174	C	GLY A 907	14.374	11.725	45.200	1.00	20.44	6227	N	SER A 915	32.382	18.019	42.461	1.00	16.85
6175	O	GLY A 907	14.554	11.417	44.029	1.00	18.16	6228	CA	SER A 915	32.568	16.964	43.470	1.00	17.87
6176	N	ASN A 908	15.070	12.662	45.868	1.00	20.78	6229	C	SER A 915	31.956	15.634	43.080	1.00	16.66
6177	CA	ASN A 908	16.156	13.320	45.167	1.00	21.15	6230	O	SER A 915	31.365	15.476	42.014	1.00	16.70
6178	C	ASN A 908	17.211	13.868	46.130	1.00	20.98	6231	CB	SER A 915	31.875	17.394	44.797	1.00	19.13
6179	O	ASN A 908	17.017	13.926	47.338	1.00	18.52	6232	OG	SER A 915	30.465	17.164	44.596	1.00	18.25
6180	CB	ASN A 908	15.571	14.503	44.390	1.00	25.44	6233	N	THR A 916	32.324	14.578	43.799	1.00	15.50
6181	CG	ASN A 908	15.149	15.737	45.145	1.00	20.00	6234	CA	THR A 916	31.790	13.243	43.594	1.00	13.88
6182	OD1	ASN A 908	14.950	16.900	44.807	1.00	20.00	6235	C	THR A 916	30.813	12.945	44.738	1.00	16.32
6183	ND2	ASN A 908	14.852	15.267	45.369	1.00	20.00	6236	O	THR A 916	31.111	13.139	45.938	1.00	16.25
6184	N	VAL A 909	18.336	14.263	45.507	1.00	18.91	6237	CB	THR A 916	32.932	12.214	43.565	1.00	15.91
6185	CA	VAL A 909	19.404	14.800	46.327	1.00	18.32	6238	OG1	THR A 916	33.805	12.538	42.444	1.00	16.29
6186	C	VAL A 909	20.288	15.881	45.643	1.00	18.88	6239	CG2	THR A 916	32.413	10.796	43.465	1.00	15.30
6187	O	VAL A 909	20.470	15.801	44.414	1.00	16.18	6240	N	LEU A 917	29.643	12.422	44.406	1.00	18.04
6188	CB	VAL A 909	20.296	13.598	46.765	1.00	17.97	6241	CA	LEU A 917	28.642	12.007	45.400	1.00	19.93
6189	CG1	VAL A 909	20.923	12.911	45.546	1.00	19.38	6242	C	LEU A 917	28.612	10.487	45.449	1.00	18.73
6190	CG2	VAL A 909	21.470	13.978	47.699	1.00	17.98	6243	O	LEU A 917	28.780	9.832	44.413	1.00	19.02
6191	N	GLN A 910	20.764	16.892	46.388	1.00	17.12	6244	CB	LEU A 917	27.290	12.536	44.972	1.00	20.24
6192	CA	GLN A 910	21.594	17.918	45.745	1.00	19.67	6245	CG	LEU A 917	26.165	12.061	45.884	1.00	20.00
6193	C	GLN A 910	23.093	17.606	45.891	1.00	20.86	6246	CD1	LEU A 917	25.876	13.041	47.022	1.00	21.86
6194	O	GLN A 910	23.536	17.338	47.015	1.00	17.07	6247	CD2	LEU A 917	24.848	11.880	45.129	1.00	20.00
6195	CB	GLN A 910	21.229	19.312	46.287	1.00	22.85	6248	N	ILE A 918	28.502	9.935	46.675	1.00	16.06

6249	CA	ILE A 918	28.452	8.487	46.780	1.00	16.89	6302	OWO WAT W 89	56.275	9.738	41.533	1.00	13.72
6250	C	ILE A 918	27.272	8.137	47.700	1.00	18.66	6303	OWO WAT W 90	69.059	-23.930	9.758	1.00	20.01
6251	O	ILE A 918	27.097	8.663	48.785	1.00	16.20	6304	OWO WAT W 91	16.344	1.857	52.262	1.00	22.62
6252	CB	ILE A 918	29.732	7.784	47.268	1.00	17.77	6305	OWO WAT W 92	75.875	-9.053	49.382	1.00	20.09
6253	CG1	ILE A 918	30.930	8.148	46.370	1.00	18.54	6306	OWO WAT W 93	76.720	-4.117	4.820	1.00	19.57
6254	CG2	ILE A 918	29.487	6.275	47.309	1.00	17.76	6307	OWO WAT W 94	32.604	16.958	29.686	1.00	15.11
6255	CD1	ILE A 918	32.249	7.494	46.754	1.00	20.20	6308	OWO WAT W 95	14.139	7.588	47.083	1.00	18.86
6256	N	LEU A 919	26.369	7.351	47.131	1.00	21.26	6309	OWO WAT W 96	39.342	-8.437	34.765	1.00	18.36
6257	CA	LEU A 919	25.184	6.865	47.783	1.00	27.90	6310	OWO WAT W 97	53.612	13.510	41.564	1.00	15.07
6258	C	LEU A 919	25.295	5.346	47.929	1.00	30.33	6311	OWO WAT W 98	36.908	-3.575	37.657	1.00	16.19
6259	O	LEU A 919	25.969	4.669	47.164	1.00	32.18	6312	OWO WAT W 99	81.997	-19.278	2.244	1.00	21.87
6260	CB	LEU A 919	23.770	7.282	47.400	1.00	25.84	6313	OWO WAT W 100	34.008	1.090	27.119	1.00	17.80
6261	CG	LEU A 919	23.523	8.755	47.030	1.00	24.77	6314	OWO WAT W 101	56.888	19.001	45.064	1.00	16.05
6262	CD1	LEU A 919	22.135	8.877	46.388	1.00	25.08	6315	OWO WAT W 102	31.113	8.775	55.007	1.00	16.75
6263	CD2	LEU A 919	23.622	9.633	48.256	1.00	24.26	6316	OWO WAT W 103	68.763	-13.614	32.213	1.00	14.83
6264	N	LYS A 920	24.551	4.859	48.938	1.00	36.42	6317	OWO WAT W 104	77.576	-15.120	38.787	1.00	17.30
6265	CA	LYS A 920	24.617	3.434	49.196	1.00	43.04	6318	OWO WAT W 105	70.975	9.008	41.415	1.00	15.80
6266	C	LYS A 920	23.193	3.022	49.576	1.00	45.32	6319	OWO WAT W 106	73.071	8.260	45.444	1.00	19.77
6267	IOCT	LYS A 920	22.398	3.801	51.035	1.00	45.54	6320	OWO WAT W 107	29.643	15.604	46.570	1.00	15.52
6268	CB	LYS A 920	25.523	2.759	50.280	1.00	44.65	6321	OWO WAT W 108	77.037	-3.080	44.844	1.00	17.45
6269	CG	LYS A 920	24.968	2.992	51.689	1.00	44.34	6322	OWO WAT W 109	71.489	-9.613	39.434	1.00	14.35
6270	CD	LYS A 920	25.851	2.376	52.776	1.00	20.00	6323	OWO WAT W 110	41.593	-4.442	45.963	1.00	18.94
6271	CE	LYS A 920	25.377	2.731	54.189	1.00	20.00	6324	OWO WAT W 111	63.736	-11.016	10.939	1.00	17.44
6272	NZ	LYS A 920	25.874	1.739	55.139	1.00	20.00	6325	OWO WAT W 112	40.024	2.255	37.806	1.00	13.52
6273	N	GLN A 921	22.682	1.858	49.773	1.00	20.00	6326	OWO WAT W 113	64.610	-1.339	34.837	1.00	14.96
6274	CA	GLN A 921	21.286	1.476	50.372	1.00	20.00	6327	OWO WAT W 114	61.987	20.548	50.028	1.00	19.83
6275	C	GLN A 921	21.261	0.073	50.618	1.00	20.00	6328	OWO WAT W 115	72.528	-7.124	29.593	1.00	18.15
6276	O	GLN A 921	22.159	-0.710	50.334	1.00	20.00	6329	OWO WAT W 116	47.271	-11.141	34.789	1.00	18.03
6277	CB	GLN A 921	19.846	1.531	49.828	1.00	20.00	6330	OWO WAT W 117	50.553	17.125	41.460	1.00	18.99
6278	CG	GLN A 921	19.352	2.234	48.564	1.00	20.00	6331	OWO WAT W 118	54.956	14.273	35.671	1.00	17.04
6279	CD	GLN A 921	18.079	1.727	47.929	1.00	20.00	6332	OWO WAT W 119	22.721	16.885	49.692	1.00	18.22
6280	OB1	GLN A 921	17.783	0.808	47.183	1.00	20.00	6333	OWO WAT W 120	68.820	9.178	39.628	1.00	15.40
6281	NE2	GLN A 921	17.165	2.459	48.597	1.00	20.00	6334	OWO WAT W 121	58.258	13.263	29.566	1.00	17.29
6282	OWO WAT W 68		69.366	-6.548	12.439	1.00	14.02	6335	OWO WAT W 122	51.860	-6.953	40.625	1.00	16.39
6283	OWO WAT W 69		32.120	-4.756	50.871	1.00	13.28	6336	OWO WAT W 123	24.503	9.804	33.921	1.00	16.52
6284	OWO WAT W 70		81.609	-10.422	31.503	1.00	15.09	6337	OWO WAT W 124	82.641	-4.698	41.936	1.00	23.28
6285	OWO WAT W 71		62.367	-0.879	37.668	1.00	12.62	6338	OWO WAT W 125	81.955	-8.160	8.351	1.00	24.39
6286	OWO WAT W 73		68.913	-12.263	29.623	1.00	13.17	6339	OWO WAT W 126	62.535	5.308	26.770	1.00	21.48
6287	OWO WAT W 74		48.063	10.500	38.858	1.00	11.72	6340	OWO WAT W 127	46.588	-10.586	39.440	1.00	17.61
6288	OWO WAT W 75		32.559	-7.482	50.485	1.00	13.66	6341	OWO WAT W 128	60.874	11.097	38.475	1.00	15.05
6289	OWO WAT W 76		32.469	1.638	38.626	1.00	14.80	6342	OWO WAT W 129	79.219	-10.342	12.004	1.00	17.14
6290	OWO WAT W 77		65.428	-1.416	31.925	1.00	11.95	6343	OWO WAT W 130	75.096	-14.661	24.693	1.00	15.31
6291	OWO WAT W 78		48.212	16.412	42.613	1.00	20.28	6344	OWO WAT W 131	37.686	29.364	40.600	1.00	21.16
6292	OWO WAT W 79		57.789	3.719	36.390	1.00	12.67	6345	OWO WAT W 132	67.581	0.034	15.638	1.00	16.05
6293	OWO WAT W 80		75.360	-12.767	22.439	1.00	15.67	6346	OWO WAT W 133	70.269	1.088	49.178	1.00	14.16
6294	OWO WAT W 81		61.875	-3.084	20.619	1.00	17.60	6347	OWO WAT W 134	77.523	-12.820	37.177	1.00	13.66
6295	OWO WAT W 82		60.223	-2.292	27.508	1.00	11.71	6348	OWO WAT W 135	77.079	-2.476	26.781	1.00	22.54
6296	OWO WAT W 83		73.802	-6.472	17.967	1.00	11.91	6349	OWO WAT W 136	44.250	-9.198	31.555	1.00	19.30
6297	OWO WAT W 84		63.768	4.437	40.319	1.00	13.88	6350	OWO WAT W 137	43.079	26.840	29.301	1.00	23.07
6298	OWO WAT W 85		36.975	5.299	53.120	1.00	17.10	6351	OWO WAT W 138	73.331	-7.883	32.692	1.00	14.37
6299	OWO WAT W 86		33.546	14.270	46.569	1.00	19.57	6352	OWO WAT W 139	70.346	8.134	44.604	1.00	19.57
6300	OWO WAT W 87		59.158	9.717	41.808	1.00	15.61	6353	OWO WAT W 140	47.819	9.959	23.729	1.00	19.80
6301	OWO WAT W 88		41.880	-1.805	42.672	1.00	18.22	6354	OWO WAT W 141	48.447	-8.906	33.755	1.00	15.32

6355	OWO WAT W 142	29.592	15.853	37.070	1.00	25.10	6408	OWO WAT W 196	68.843	-18.109	15.825	1.00	22.65
6356	OWO WAT W 143	45.897	-14.006	-16.368	1.00	21.95	6409	OWO WAT W 197	18.045	9.415	37.687	1.00	23.22
6357	OWO WAT W 144	65.522	5.063	38.083	1.00	12.12	6410	OWO WAT W 198	19.821	3.539	53.464	1.00	25.47
6358	OWO WAT W 145	67.211	0.550	32.731	1.00	17.01	6411	OWO WAT W 199	37.934	-8.358	42.258	1.00	22.96
6359	OWO WAT W 146	58.188	15.032	33.459	1.00	18.01	6412	OWO WAT W 200	66.324	-17.028	33.133	1.00	21.67
6360	OWO WAT W 147	56.888	-10.260	18.807	1.00	24.03	6413	OWO WAT W 201	89.568	-0.730	43.526	1.00	39.85
6361	OWO WAT W 148	69.862	-15.067	24.194	1.00	12.26	6414	OWO WAT W 202	65.791	-8.953	56.239	1.00	24.77
6362	OWO WAT W 149	66.848	18.769	50.441	1.00	26.40	6415	OWO WAT W 203	30.336	-3.688	-15.714	1.00	31.23
6363	OWO WAT W 150	39.850	10.596	24.937	1.00	15.47	6416	OWO WAT W 204	38.412	2.069	31.675	1.00	14.46
6364	OWO WAT W 151	46.212	-0.290	4.537	1.00	19.55	6417	OWO WAT W 205	48.840	-16.134	30.302	1.00	22.40
6365	OWO WAT W 152	69.349	10.471	29.638	1.00	25.61	6418	OWO WAT W 206	66.775	20.286	40.341	1.00	25.65
6366	OWO WAT W 153	75.556	-7.180	31.034	1.00	17.73	6419	OWO WAT W 207	37.823	3.881	27.553	1.00	16.42
6367	OWO WAT W 154	77.494	-24.179	15.886	1.00	19.43	6420	OWO WAT W 208	51.918	25.040	45.285	1.00	35.74
6368	OWO WAT W 155	62.259	12.967	49.436	1.00	16.99	6421	OWO WAT W 209	57.850	21.185	46.630	1.00	23.05
6369	OWO WAT W 157	81.536	-10.806	5.685	1.00	17.76	6422	OWO WAT W 210	20.044	17.034	49.140	1.00	14.24
6370	OWO WAT W 158	62.854	-16.944	21.280	1.00	30.32	6423	OWO WAT W 211	71.715	-5.894	10.737	1.00	16.38
6371	OWO WAT W 159	47.815	-3.762	-20.195	1.00	24.16	6424	OWO WAT W 212	66.725	-5.950	11.424	1.00	25.24
6372	OWO WAT W 160	74.332	-2.627	26.574	1.00	20.89	6425	OWO WAT W 213	69.977	-19.080	28.620	1.00	22.47
6373	OWO WAT W 161	73.134	-8.343	11.701	1.00	14.37	6426	OWO WAT W 214	41.220	-1.629	45.498	1.00	14.57
6374	OWO WAT W 162	35.562	-10.370	30.256	1.00	16.76	6427	OWO WAT W 215	80.849	-10.168	9.676	1.00	15.11
6375	OWO WAT W 163	89.451	-13.445	20.007	1.00	17.74	6428	OWO WAT W 216	65.460	-4.423	5.582	1.00	25.44
6376	OWO WAT W 164	64.437	-8.353	11.350	1.00	19.87	6429	OWO WAT W 217	60.371	3.984	54.712	1.00	19.11
6377	OWO WAT W 165	42.448	-1.014	52.692	1.00	25.22	6430	OWO WAT W 218	46.146	-14.480	-19.119	1.00	22.68
6378	OWO WAT W 166	46.191	-7.466	32.597	1.00	19.58	6431	OWO WAT W 220	75.425	-5.678	28.718	1.00	14.44
6379	OWO WAT W 167	74.558	-4.139	51.689	1.00	21.48	6432	OWO WAT W 221	64.613	5.872	48.455	1.00	15.74
6380	OWO WAT W 168	58.355	12.098	38.036	1.00	18.33	6433	OWO WAT W 222	76.468	4.175	45.089	1.00	15.34
6381	OWO WAT W 169	64.827	20.010	32.662	1.00	24.95	6434	OWO WAT W 223	78.530	-3.248	30.018	1.00	18.35
6382	OWO WAT W 170	46.993	18.543	20.841	1.00	20.41	6435	OWO WAT W 224	66.447	-15.601	45.227	1.00	21.57
6383	OWO WAT W 171	35.631	21.698	36.640	1.00	16.68	6436	OWO WAT W 225	64.601	13.864	43.344	1.00	19.79
6384	OWO WAT W 172	54.527	4.577	34.040	1.00	16.16	6437	OWO WAT W 226	84.129	-21.451	40.447	1.00	23.07
6385	OWO WAT W 173	79.048	-13.312	16.275	1.00	19.28	6438	OWO WAT W 227	50.240	9.246	25.360	1.00	27.34
6386	OWO WAT W 174	34.755	5.781	57.522	1.00	28.62	6439	OWO WAT W 228	71.340	-3.838	2.003	1.00	28.41
6387	OWO WAT W 175	24.290	-8.263	41.358	1.00	27.30	6440	OWO WAT W 229	85.282	-20.669	0.886	1.00	31.69
6388	OWO WAT W 176	43.005	20.391	32.602	1.00	20.84	6441	OWO WAT W 230	26.568	-10.850	46.117	1.00	21.74
6389	OWO WAT W 177	30.870	-2.649	54.736	1.00	25.48	6442	OWO WAT W 231	70.878	-18.207	31.358	1.00	23.68
6390	OWO WAT W 178	53.261	8.959	50.601	1.00	24.03	6443	OWO WAT W 232	35.309	24.294	36.012	1.00	20.39
6391	OWO WAT W 179	53.517	5.558	31.784	1.00	24.92	6444	OWO WAT W 233	52.580	4.977	18.388	1.00	22.44
6392	OWO WAT W 180	68.153	-15.586	16.468	1.00	17.73	6445	OWO WAT W 234	50.557	11.295	58.608	1.00	20.04
6393	OWO WAT W 181	80.333	-14.549	-8.414	1.00	28.75	6446	OWO WAT W 235	23.949	20.846	34.191	1.00	26.29
6394	OWO WAT W 182	77.155	4.046	42.470	1.00	16.63	6447	OWO WAT W 236	35.623	14.411	43.636	1.00	19.95
6395	OWO WAT W 183	36.194	17.220	43.863	1.00	17.32	6448	OWO WAT W 237	64.405	-7.438	8.777	1.00	24.16
6396	OWO WAT W 184	74.883	3.842	36.360	1.00	18.34	6449	OWO WAT W 238	75.075	-15.366	34.214	1.00	24.35
6397	OWO WAT W 185	43.383	31.022	45.350	1.00	34.65	6450	OWO WAT W 239	49.008	-14.858	26.445	1.00	18.45
6398	OWO WAT W 186	55.792	6.996	60.761	1.00	19.70	6451	OWO WAT W 240	67.130	18.121	47.777	1.00	26.38
6399	OWO WAT W 187	62.221	10.100	60.967	1.00	17.41	6452	OWO WAT W 241	58.462	-8.275	-6.771	1.00	27.46
6400	OWO WAT W 188	72.467	-14.137	23.905	1.00	18.11	6453	OWO WAT W 242	89.032	-3.538	32.201	1.00	37.77
6401	OWO WAT W 189	43.775	-10.296	29.108	1.00	13.72	6454	OWO WAT W 243	76.413	-9.886	12.043	1.00	19.59
6402	OWO WAT W 190	46.321	8.776	37.734	1.00	17.82	6455	OWO WAT W 244	91.058	-23.122	27.002	1.00	29.55
6403	OWO WAT W 191	58.197	4.756	57.467	1.00	18.48	6456	OWO WAT W 245	68.897	-16.420	32.353	1.00	17.73
6404	OWO WAT W 192	18.946	19.472	50.053	1.00	43.73	6457	OWO WAT W 246	60.787	20.118	45.579	1.00	19.06
6405	OWO WAT W 193	46.641	23.645	40.314	1.00	15.11	6458	OWO WAT W 247	57.295	9.602	38.862	1.00	18.19
6406	OWO WAT W 194	73.073	2.447	2.145	1.00	25.40	6459	OWO WAT W 248	51.834	13.502	33.252	1.00	16.33
6407	OWO WAT W 195	69.006	20.130	42.674	1.00	29.03	6460	OWO WAT W 250	37.078	29.140	45.806	1.00	19.44

6461	OWO	WAT	W 251	79.365	-4.623	6.311	1.00	27.30	6514	OWO	WAT	W 304	50.616	-5.935	44.803	1.00	18.59
6462	OWO	WAT	W 252	50.994	3.684	58.665	1.00	26.14	6515	OWO	WAT	W 305	77.962	12.398	43.121	1.00	32.94
6463	OWO	WAT	W 253	16.237	1.326	45.058	1.00	21.57	66.149	OWO	WAT	W 306	-13.682	-12.914	1.00	28.81	
6464	OWO	WAT	W 254	59.347	18.360	43.822	1.00	21.00	6517	OWO	WAT	W 307	82.412	-2.518	2.943	1.00	26.24
6465	OWO	WAT	W 255	93.718	-8.612	37.885	1.00	27.72	6518	OWO	WAT	W 308	37.840	23.041	26.322	1.00	28.62
6466	OWO	WAT	W 256	18.476	13.116	37.804	1.00	20.53	6519	OWO	WAT	W 309	61.723	-12.439	11.952	1.00	27.68
6467	OWO	WAT	W 257	74.988	-1.264	7.841	1.00	23.15	45.805	OWO	WAT	W 310	45.805	-15.302	29.600	1.00	42.22
6468	OWO	WAT	W 258	65.708	-9.485	2.882	1.00	24.47	6521	OWO	WAT	W 311	37.738	11.900	54.333	1.00	30.73
6469	OWO	WAT	W 259	81.228	-18.556	15.613	1.00	21.70	6522	OWO	WAT	W 312	78.463	-14.147	-10.311	1.00	23.91
6470	OWO	WAT	W 260	40.153	18.506	50.014	1.00	29.11	6523	OWO	WAT	W 313	46.583	-15.364	34.986	1.00	23.46
6471	OWO	WAT	W 261	76.275	-15.000	27.216	1.00	14.07	6524	OWO	WAT	W 314	62.766	5.097	12.438	1.00	22.65
6472	OWO	WAT	W 262	32.653	-11.672	30.238	1.00	24.10	6525	OWO	WAT	W 315	43.230	0.820	-21.984	1.00	35.81
6473	OWO	WAT	W 263	33.719	19.637	32.612	1.00	23.35	6526	OWO	WAT	W 316	43.950	4.358	-15.650	1.00	23.67
6474	OWO	WAT	W 264	57.975	6.308	29.825	1.00	28.17	6527	OWO	WAT	W 317	42.859	-10.546	45.639	1.00	32.28
6475	OWO	WAT	W 265	56.014	3.037	13.415	1.00	27.45	6528	OWO	WAT	W 318	49.162	-3.978	1.765	1.00	43.38
6476	OWO	WAT	W 266	35.289	-10.133	-21.987	1.00	24.36	6529	OWO	WAT	W 319	60.903	21.253	54.960	1.00	32.40
6477	OWO	WAT	W 267	48.772	-1.478	-18.710	1.00	22.08	6530	OWO	WAT	W 320	84.179	-7.984	18.419	1.00	21.93
6478	OWO	WAT	W 268	56.907	-15.816	-21.447	1.00	21.69	6531	OWO	WAT	W 321	44.701	-15.753	-5.792	1.00	24.15
6479	OWO	WAT	W 269	70.103	-9.623	56.538	1.00	21.05	6532	OWO	WAT	W 322	17.649	6.695	35.037	1.00	33.00
6480	OWO	WAT	W 270	66.182	8.595	31.274	1.00	23.04	6533	OWO	WAT	W 323	39.424	-10.529	42.109	1.00	24.43
6481	OWO	WAT	W 271	43.509	-7.089	-19.497	1.00	25.51	6534	OWO	WAT	W 324	17.053	-3.033	44.924	1.00	32.20
6482	OWO	WAT	W 272	75.559	-23.596	13.036	1.00	25.28	6535	OWO	WAT	W 325	71.659	-19.394	34.189	1.00	39.67
6483	OWO	WAT	W 273	52.581	11.622	50.505	1.00	19.81	6536	OWO	WAT	W 326	60.464	-11.885	54.688	1.00	29.00
6484	OWO	WAT	W 274	70.407	-23.742	7.358	1.00	26.46	6537	OWO	WAT	W 327	60.150	8.501	29.954	1.00	22.12
6485	OWO	WAT	W 275	47.060	18.265	28.697	1.00	32.17	6538	OWO	WAT	W 328	71.908	12.459	33.945	1.00	31.00
6486	OWO	WAT	W 276	45.135	20.614	54.368	1.00	26.24	6539	OWO	WAT	W 329	50.518	-6.710	-4.970	1.00	24.35
6487	OWO	WAT	W 277	78.588	-20.221	12.456	1.00	28.74	6540	OWO	WAT	W 330	81.378	-2.927	27.039	1.00	28.44
6488	OWO	WAT	W 278	26.272	-3.352	44.999	1.00	18.45	6541	OWO	WAT	W 331	69.282	-16.298	45.601	1.00	27.45
6489	OWO	WAT	W 279	27.844	23.521	45.472	1.00	19.15	6542	OWO	WAT	W 332	67.427	-13.423	-6.333	1.00	30.02
6490	OWO	WAT	W 280	43.415	-9.483	-20.814	1.00	22.24	6543	OWO	WAT	W 333	46.329	-12.182	37.298	1.00	20.51
6491	OWO	WAT	W 281	44.928	-9.823	21.085	1.00	21.62	6544	OWO	WAT	W 334	48.718	-20.006	-14.082	1.00	29.70
6492	OWO	WAT	W 282	67.718	4.640	5.963	1.00	25.19	6545	OWO	WAT	W 335	43.754	-13.207	36.811	1.00	26.82
6493	OWO	WAT	W 283	96.982	-10.458	37.245	1.00	30.81	6546	OWO	WAT	W 336	64.098	14.236	26.166	1.00	29.05
6494	OWO	WAT	W 284	48.457	4.929	-7.033	1.00	23.97	6547	OWO	WAT	W 337	37.049	3.266	-19.372	1.00	31.08
6495	OWO	WAT	W 285	55.985	-7.377	-3.129	1.00	27.03	6548	OWO	WAT	W 338	61.795	-10.158	-4.790	1.00	34.78
6496	OWO	WAT	W 286	35.786	-2.048	0.183	1.00	30.57	6549	OWO	WAT	W 339	49.037	0.420	51.729	1.00	23.15
6497	OWO	WAT	W 287	78.219	-5.390	40.921	1.00	16.49	6550	OWO	WAT	W 340	75.001	-18.929	4.449	1.00	25.65
6498	OWO	WAT	W 288	77.364	-21.161	31.334	1.00	18.15	6551	OWO	WAT	W 341	65.358	-16.321	0.957	1.00	30.48
6499	OWO	WAT	W 289	50.808	-19.872	31.259	1.00	23.98	6552	OWO	WAT	W 342	42.464	13.861	23.091	1.00	28.92
6500	OWO	WAT	W 290	31.863	-12.519	43.355	1.00	21.97	6553	OWO	WAT	W 343	88.313	-2.838	44.183	1.00	29.50
6501	OWO	WAT	W 291	49.112	-1.399	15.411	1.00	32.14	6554	OWO	WAT	W 344	32.606	12.506	24.842	1.00	22.59
6502	OWO	WAT	W 292	36.747	2.739	53.684	1.00	28.77	6555	OWO	WAT	W 345	56.691	16.693	46.428	1.00	23.81
6503	OWO	WAT	W 293	47.932	-3.952	50.396	1.00	29.44	6556	OWO	WAT	W 346	91.741	-3.418	41.436	1.00	31.63
6504	OWO	WAT	W 294	75.259	-18.091	42.038	1.00	27.99	6557	OWO	WAT	W 347	41.803	11.235	23.103	1.00	38.16
6505	OWO	WAT	W 295	65.026	17.315	32.530	1.00	25.64	6558	OWO	WAT	W 348	46.070	-13.919	32.782	1.00	29.90
6506	OWO	WAT	W 296	78.244	-25.283	12.611	1.00	35.84	6559	OWO	WAT	W 349	54.505	-7.501	-20.473	1.00	30.31
6507	OWO	WAT	W 297	85.182	-4.003	27.099	1.00	38.09	6560	OWO	WAT	W 350	80.666	-8.291	47.313	1.00	31.98
6508	OWO	WAT	W 298	58.707	-10.508	52.943	1.00	20.88	6561	OWO	WAT	W 351	72.442	3.961	-1.194	1.00	29.66
6509	OWO	WAT	W 299	51.111	17.227	31.022	1.00	29.87	6562	OWO	WAT	W 352	37.415	6.655	27.782	1.00	26.05
6510	OWO	WAT	W 300	61.340	-13.950	17.572	1.00	27.41	6563	OWO	WAT	W 353	68.123	-17.644	51.248	1.00	32.02
6511	OWO	WAT	W 301	38.209	-3.845	-22.771	1.00	26.19	6564	OWO	WAT	W 354	61.089	23.461	40.340	1.00	27.24
6512	OWO	WAT	W 302	72.914	-22.668	6.220	1.00	26.26	6565	OWO	WAT	W 355	19.026	-6.909	51.121	1.00	26.68
6513	OWO	WAT	W 303	66.840	-21.476	4.405	1.00	27.43	6566	OWO	WAT	W 356	34.952	4.204	-5.390	1.00	33.99

6567	OWO	WAT	W 357	44.994	-11.459	33.261	1.00	25.35	6620	OWO	WAT	W 411	25.339	-10.076	43.114	1.00	23.49
6568	OWO	WAT	W 358	45.207	-6.145	46.236	1.00	25.52	6621	OWO	WAT	W 412	66.204	-5.949	25.409	1.00	30.80
6569	OWO	WAT	W 359	40.573	15.286	24.984	1.00	28.94	6622	OWO	WAT	W 413	38.412	-12.030	33.503	1.00	27.23
6570	OWO	WAT	W 361	72.962	2.265	55.757	1.00	26.75	6623	OWO	WAT	W 414	33.850	28.896	42.331	1.00	47.21
6571	OWO	WAT	W 362	71.459	-26.046	4.160	1.00	28.61	6624	OWO	WAT	W 415	17.795	16.340	37.828	1.00	33.59
6572	OWO	WAT	W 363	38.402	20.036	48.661	1.00	22.55	6625	OWO	WAT	W 416	34.565	-12.132	23.818	1.00	31.86
6573	OWO	WAT	W 364	32.615	21.884	33.926	1.00	31.74	6626	OWO	WAT	W 417	91.832	-14.160	17.359	1.00	37.03
6574	OWO	WAT	W 365	80.451	-4.586	48.849	1.00	25.59	6627	OWO	WAT	W 418	47.439	14.844	32.551	1.00	33.39
6575	OWO	WAT	W 366	73.839	-20.204	6.685	1.00	23.97	6628	OWO	WAT	W 419	69.434	-25.542	21.203	1.00	41.60
6576	OWO	WAT	W 367	79.652	-24.057	29.577	1.00	25.40	6629	OWO	WAT	W 420	55.830	-14.109	41.979	1.00	51.22
6577	OWO	WAT	W 368	49.566	13.147	31.160	1.00	38.08	6630	OWO	WAT	W 421	42.926	-12.881	34.347	1.00	23.83
6578	OWO	WAT	W 369	38.584	8.766	23.418	1.00	24.62	6631	OWO	WAT	W 422	63.743	-0.676	4.790	1.00	36.35
6579	OWO	WAT	W 370	77.248	-23.896	30.696	1.00	25.85	6632	OWO	WAT	W 423	55.526	0.391	11.719	1.00	43.19
6580	OWO	WAT	W 371	77.989	-20.493	8.093	1.00	28.17	6633	OWO	WAT	W 424	73.417	12.097	49.004	1.00	38.46
6581	OWO	WAT	W 372	47.120	-18.023	33.871	1.00	30.24	6634	OWO	WAT	W 425	52.369	24.730	35.218	1.00	28.92
6582	OWO	WAT	W 373	10.465	5.660	47.993	1.00	36.55	6635	OWO	WAT	W 426	62.668	-12.567	-11.718	1.00	28.63
6583	OWO	WAT	W 374	57.307	14.254	27.302	1.00	27.17	6636	OWO	WAT	W 427	64.528	-14.519	-11.603	1.00	34.77
6584	OWO	WAT	W 375	38.985	13.275	24.929	1.00	23.57	6637	OWO	WAT	W 428	85.369	-26.700	28.869	1.00	34.96
6585	OWO	WAT	W 376	72.047	-16.693	37.366	1.00	32.15	6638	OWO	WAT	W 429	34.890	11.971	56.023	1.00	30.32
6586	OWO	WAT	W 377	47.471	4.237	-17.052	1.00	36.00	6639	OWO	WAT	W 430	38.319	13.761	52.914	1.00	38.81
6587	OWO	WAT	W 378	51.129	-18.579	-13.092	1.00	23.58	6640	OWO	WAT	W 431	36.205	-3.725	22.946	1.00	38.51
6588	OWO	WAT	W 379	86.696	-24.221	18.981	1.00	29.96	6641	OWO	WAT	W 432	61.755	-18.698	19.722	1.00	32.41
6589	OWO	WAT	W 380	85.791	-0.516	37.710	1.00	29.15	6642	OWO	WAT	W 433	73.740	-17.674	33.635	1.00	36.99
6590	OWO	WAT	W 381	84.814	-13.838	11.838	1.00	25.35	6643	OWO	WAT	W 434	62.176	-18.812	26.590	1.00	35.56
6591	OWO	WAT	W 382	28.157	-11.801	44.088	1.00	22.15	6644	OWO	WAT	W 435	80.166	-4.065	15.814	1.00	41.24
6592	OWO	WAT	W 383	62.926	22.843	35.656	1.00	35.59	6645	OWO	WAT	W 436	63.537	-3.108	10.225	1.00	26.01
6593	OWO	WAT	W 384	17.572	0.721	42.711	1.00	25.43	6646	OWO	WAT	W 437	70.855	11.063	55.846	1.00	38.80
6594	OWO	WAT	W 385	75.014	-27.098	16.437	1.00	28.81	6647	OWO	WAT	W 438	55.025	19.284	36.156	1.00	21.38
6595	OWO	WAT	W 386	67.132	-16.141	-2.946	1.00	32.78	6648	OWO	WAT	W 439	82.953	-0.517	19.836	1.00	31.57
6596	OWO	WAT	W 387	22.477	9.654	59.781	1.00	34.92	6649	OWO	WAT	W 440	77.888	3.005	35.260	1.00	27.61
6597	OWO	WAT	W 388	28.624	-2.581	27.502	1.00	40.90	6650	OWO	WAT	W 441	47.174	-19.776	-25.723	1.00	25.70
6598	OWO	WAT	W 389	68.480	5.583	25.870	1.00	20.19	6651	OWO	WAT	W 442	15.282	-0.724	48.333	1.00	63.95
6599	OWO	WAT	W 390	72.335	-15.678	52.469	1.00	24.90	6652	OWO	WAT	W 443	45.668	2.364	56.289	1.00	29.20
6600	OWO	WAT	W 391	72.401	9.938	47.835	1.00	38.08	6653	OWO	WAT	W 444	55.704	7.505	11.701	1.00	31.83
6601	OWO	WAT	W 392	37.136	-4.896	3.579	1.00	39.22	6654	OWO	WAT	W 445	41.558	6.741	55.087	1.00	34.44
6602	OWO	WAT	W 393	87.130	-3.587	22.928	1.00	28.96	6655	OWO	WAT	W 446	73.701	7.136	28.230	1.00	26.54
6603	OWO	WAT	W 394	59.733	21.534	42.236	1.00	19.04	6656	OWO	WAT	W 447	21.624	11.628	31.608	1.00	30.60
6604	OWO	WAT	W 395	49.614	-6.092	47.633	1.00	26.38	6657	OWO	WAT	W 448	97.126	-16.727	30.310	1.00	34.64
6605	OWO	WAT	W 396	68.508	-18.979	0.775	1.00	25.22	6658	OWO	WAT	W 449	74.340	-4.743	24.963	1.00	45.37
6606	OWO	WAT	W 397	30.344	16.345	53.767	1.00	21.53	6659	OWO	WAT	W 450	84.402	-6.560	16.139	1.00	30.72
6607	OWO	WAT	W 398	36.689	-10.063	44.341	1.00	27.75	6660	OWO	WAT	W 451	28.262	21.244	24.604	1.00	43.08
6608	OWO	WAT	W 399	44.255	10.317	20.950	1.00	38.55	6661	OWO	WAT	W 452	23.084	1.809	31.647	1.00	26.48
6609	OWO	WAT	W 400	80.351	-27.377	31.973	1.00	29.96	6662	OWO	WAT	W 453	42.394	-4.193	3.333	1.00	31.81
6610	OWO	WAT	W 401	62.323	-7.884	-10.201	1.00	25.19	6663	OWO	WAT	W 454	62.371	-1.473	8.394	1.00	27.83
6611	OWO	WAT	W 402	48.124	-18.230	-10.307	1.00	28.48	6664	OWO	WAT	W 455	46.837	6.251	21.345	1.00	36.13
6612	OWO	WAT	W 403	61.453	-14.796	-18.703	1.00	40.45	6665	OWO	WAT	W 456	35.480	26.992	45.795	1.00	28.88
6613	OWO	WAT	W 404	66.241	-21.530	28.934	1.00	30.44	6666	OWO	WAT	W 457	51.976	-7.138	-1.858	1.00	31.75
6614	OWO	WAT	W 405	39.152	22.713	47.906	1.00	17.90	6667	OWO	WAT	W 458	69.604	-18.226	42.817	1.00	31.57
6615	OWO	WAT	W 406	46.042	-16.832	-9.093	1.00	35.13	6668	OWO	WAT	W 459	68.233	-16.493	-13.125	1.00	34.37
6616	OWO	WAT	W 407	63.039	0.557	60.763	1.00	33.78	6669	OWO	WAT	W 460	38.919	4.604	-15.945	1.00	30.77
6617	OWO	WAT	W 408	64.512	10.494	17.998	1.00	31.21	6670	OWO	WAT	W 461	54.603	-1.784	-10.268	1.00	29.83
6618	OWO	WAT	W 409	66.376	-17.542	55.784	1.00	21.41	6671	OWO	WAT	W 462	75.522	-18.796	38.966	1.00	35.67
6619	OWO	WAT	W 410	47.053	-15.752	-6.786	1.00	27.55	6672	OWO	WAT	W 463	81.655	-2.401	17.151	1.00	32.07

6673	OWO	WAT	W 464	57.826	-19.166	25.096	1.00	38.97	6726	OWO	WAT	W 517	88.040	-1.843	36.126	1.00	30.26
6674	OWO	WAT	W 465	81.263	-20.540	14.119	1.00	33.94	6727	OWO	WAT	W 518	71.250	15.795	48.528	1.00	29.38
6675	OWO	WAT	W 466	63.386	-6.403	6.370	1.00	39.46	6728	OWO	WAT	W 520	15.848	7.343	57.167	1.00	32.22
6676	OWO	WAT	W 467	81.257	0.044	-1.327	1.00	37.79	6729	OWO	WAT	W 521	34.398	-21.215	-9.737	1.00	44.50
6677	OWO	WAT	W 468	46.062	-15.455	-25.516	1.00	41.40	6730	OWO	WAT	W 522	64.038	-6.164	54.619	1.00	32.76
6678	OWO	WAT	W 469	20.247	20.109	38.622	1.00	27.65	6731	OWO	WAT	W 523	64.354	1.072	-3.179	1.00	29.78
6679	OWO	WAT	W 470	77.490	-21.509	14.231	1.00	36.26	6732	OWO	WAT	W 524	85.120	3.839	36.045	1.00	40.08
6680	OWO	WAT	W 471	76.196	-24.636	0.276	1.00	43.65	6733	OWO	WAT	W 525	86.257	2.953	41.138	1.00	41.59
6681	OWO	WAT	W 472	30.399	24.885	35.289	1.00	33.93	6734	OWO	WAT	W 526	52.892	6.449	29.807	1.00	29.56
6682	OWO	WAT	W 473	30.055	13.347	25.308	1.00	32.70	6735	OWO	WAT	W 527	44.099	5.976	-11.549	1.00	27.68
6683	OWO	WAT	W 474	84.910	-4.142	0.423	1.00	39.08	6736	OWO	WAT	W 528	54.883	-0.564	-7.820	1.00	28.79
6684	OWO	WAT	W 475	31.259	0.007	-12.949	1.00	31.64	6737	OWO	WAT	W 529	80.659	-25.958	36.000	1.00	43.82
6685	OWO	WAT	W 476	36.835	26.993	49.651	1.00	27.17	6738	OWO	WAT	W 530	77.061	-1.218	13.093	1.00	33.25
6686	OWO	WAT	W 477	90.488	-25.441	33.765	1.00	38.57	6739	OWO	WAT	W 531	12.960	2.681	41.428	1.00	40.30
6687	OWO	WAT	W 478	58.971	15.316	62.875	1.00	38.57	6740	OWO	WAT	W 532	15.085	14.951	49.204	1.00	33.19
6688	OWO	WAT	W 479	71.338	-25.348	1.040	1.00	55.72	6741	OWO	WAT	W 533	66.186	-17.851	36.224	1.00	44.47
6689	OWO	WAT	W 480	41.705	-19.415	-13.619	1.00	37.68	6742	OWO	WAT	W 534	33.556	-7.708	-22.528	1.00	36.36
6690	OWO	WAT	W 481	69.730	14.867	50.512	1.00	26.27	6743	OWO	WAT	W 535	64.789	-11.150	5.378	1.00	30.63
6691	OWO	WAT	W 482	14.828	13.346	51.319	1.00	27.62	6744	OWO	WAT	W 536	60.271	6.086	27.464	1.00	32.06
6692	OWO	WAT	W 483	90.856	-21.318	-3.133	1.00	53.86	6745	OWO	WAT	W 537	90.487	-15.669	14.264	1.00	35.70
6693	OWO	WAT	W 484	56.183	-9.627	16.617	1.00	30.41	6746	OWO	WAT	W 538	79.423	-0.659	26.417	1.00	32.62
6694	OWO	WAT	W 485	57.382	-1.553	-6.767	1.00	29.36	6747	OWO	WAT	W 539	77.499	-9.225	41.241	1.00	38.84
6695	OWO	WAT	W 486	37.727	-6.554	-23.027	1.00	31.09	6748	OWO	WAT	W 540	38.460	-17.144	-22.854	1.00	32.97
6696	OWO	WAT	W 487	60.051	24.897	33.921	1.00	48.03	6749	OWO	WAT	W 541	95.109	-18.447	21.117	1.00	45.20
6697	OWO	WAT	W 488	17.634	15.818	50.213	1.00	46.53	6750	OWO	WAT	W 542	46.885	1.862	-21.845	1.00	45.25
6698	OWO	WAT	W 489	78.778	-24.898	44.836	1.00	40.33	6751	OWO	WAT	W 543	72.300	15.489	37.082	1.00	38.81
6699	OWO	WAT	W 490	65.719	9.772	60.623	1.00	47.51	6752	OWO	WAT	W 544	53.484	-19.303	24.437	1.00	31.94
6700	OWO	WAT	W 491	21.583	-9.599	41.401	1.00	37.21	6753	OWO	WAT	W 545	68.271	-16.075	53.457	1.00	33.31
6701	OWO	WAT	W 492	47.040	2.603	20.841	1.00	34.24	6754	OWO	WAT	W 546	81.187	-12.562	8.492	1.00	31.48
6702	OWO	WAT	W 493	54.279	1.535	-18.697	1.00	44.41	6755	OWO	WAT	W 547	49.103	-15.891	43.116	1.00	33.62
6703	OWO	WAT	W 494	62.066	-1.934	-8.477	1.00	39.01	6756	OWO	WAT	W 548	63.252	-20.824	18.880	1.00	38.97
6704	OWO	WAT	W 495	30.722	-7.382	-7.418	1.00	34.70	6757	OWO	WAT	W 549	86.032	-2.093	25.031	1.00	38.83
6705	OWO	WAT	W 496	31.310	1.784	-6.926	1.00	31.46	6758	OWO	WAT	W 550	50.812	-9.392	-2.366	1.00	32.70
6706	OWO	WAT	W 497	52.330	11.012	30.962	1.00	32.49	6759	OWO	WAT	W 551	77.222	-22.310	5.262	1.00	42.02
6707	OWO	WAT	W 498	65.945	-20.083	21.418	1.00	30.34	6760	OWO	WAT	W 552	87.105	0.417	40.246	1.00	33.75
6708	OWO	WAT	W 499	50.770	-10.173	12.866	1.00	47.95	6761	OWO	WAT	W 553	39.779	-10.913	28.103	1.00	32.23
6709	OWO	WAT	W 500	61.046	23.935	37.360	1.00	32.34	6762	OWO	WAT	W 554	80.530	5.700	44.684	1.00	22.37
6710	OWO	WAT	W 501	39.600	2.991	-0.996	1.00	46.45	6763	OWO	WAT	W 555	44.445	21.933	51.741	1.00	40.68
6711	OWO	WAT	W 502	27.724	-11.311	40.533	1.00	16.56	6764	OWO	WAT	W 556	78.037	4.895	33.580	1.00	38.94
6712	OWO	WAT	W 503	59.536	-2.849	-8.699	1.00	28.34	6765	OWO	WAT	W 557	50.785	-1.091	53.731	1.00	40.29
6713	OWO	WAT	W 504	40.735	24.000	49.923	1.00	34.03	6766	OWO	WAT	W 558	48.427	-18.608	31.494	1.00	38.93
6714	OWO	WAT	W 505	73.997	-27.214	14.115	1.00	43.47	6767	OWO	WAT	W 559	36.861	8.729	55.912	1.00	32.41
6715	OWO	WAT	W 506	40.887	-10.965	33.589	1.00	26.99	6768	OWO	WAT	W 560	34.764	8.292	57.897	1.00	41.50
6716	OWO	WAT	W 507	82.531	3.559	45.765	1.00	30.67	6769	OWO	WAT	W 561	52.719	-18.428	-15.193	1.00	34.83
6717	OWO	WAT	W 508	48.547	-17.731	-5.638	1.00	44.65	6770	OWO	WAT	W 562	21.141	21.506	43.413	1.00	35.68
6718	OWO	WAT	W 509	40.883	-5.002	48.490	1.00	31.16	6771	OWO	WAT	W 563	32.675	10.931	22.641	1.00	33.70
6719	OWO	WAT	W 510	76.430	-25.387	32.925	1.00	30.36	6772	OWO	WAT	W 564	79.498	-28.457	28.133	1.00	41.72
6720	OWO	WAT	W 511	71.990	12.764	51.191	1.00	30.30	6773	OWO	WAT	W 565	31.047	-13.425	34.555	1.00	32.76
6721	OWO	WAT	W 512	20.681	0.962	54.358	1.00	33.83	6774	OWO	WAT	W 566	17.333	-4.663	51.771	1.00	23.15
6722	OWO	WAT	W 513	27.139	25.062	36.224	1.00	39.95	6775	OWO	WAT	W 567	73.981	-25.793	-1.995	1.00	46.66
6723	OWO	WAT	W 514	83.997	-20.448	13.120	1.00	46.83	6776	OWO	WAT	W 568	54.933	7.887	31.452	1.00	35.09
6724	OWO	WAT	W 515	79.230	-24.653	37.743	1.00	35.45	6777	OWO	WAT	W 569	40.812	-13.172	37.899	1.00	34.36
6725	OWO	WAT	W 516	38.032	-10.688	-25.566	1.00	31.11	6778	OWO	WAT	W 570	90.118	-22.677	43.385	1.00	42.30

6779	OWO WAT W 571	49.795	16.333	32.935	1.00	33.34	6832	OWO WAT W 626	95.260	-15.509	41.378	1.00	32.64
6780	OWO WAT W 572	86.224	-3.103	29.568	1.00	45.18	6833	OWO WAT W 627	60.917	-1.177	13.410	1.00	40.04
6781	OWO WAT W 573	93.985	-21.583	25.927	1.00	49.38	6834	OWO WAT W 628	60.376	-14.353	56.761	1.00	47.88
6782	OWO WAT W 574	48.711	29.216	31.209	1.00	38.64	6835	OWO WAT W 629	35.528	-17.752	20.354	1.00	38.18
6783	OWO WAT W 575	80.779	-26.481	29.557	1.00	41.33	6836	OWO WAT W 630	53.084	17.303	25.669	1.00	46.68
6784	OWO WAT W 576	30.291	-0.331	-3.469	1.00	33.78	6837	OWO WAT W 631	49.338	24.584	23.434	1.00	37.08
6785	OWO WAT W 577	83.004	-7.012	12.342	1.00	54.12	6838	OWO WAT W 632	44.633	31.369	41.827	1.00	51.68
6786	OWO WAT W 578	77.402	10.589	36.940	1.00	34.01	6839	OWO WAT W 633	41.364	9.274	55.363	1.00	48.19
6787	OWO WAT W 579	36.261	17.002	46.660	1.00	36.83	6840	OWO WAT W 634	85.480	-8.670	45.623	1.00	38.50
6788	OWO WAT W 580	72.862	13.977	47.223	1.00	31.19	6841	OWO WAT W 635	67.366	8.090	27.660	1.00	46.28
6789	OWO WAT W 581	47.939	-15.855	24.111	1.00	32.81	6842	OWO WAT W 636	58.044	20.208	61.858	1.00	43.81
6790	OWO WAT W 582	77.692	6.100	24.255	1.00	39.63	6843	OWO WAT W 637	60.247	-6.665	-19.077	1.00	33.84
6791	OWO WAT W 583	64.653	-13.766	4.879	1.00	38.84	6844	OWO WAT W 638	22.729	2.441	55.615	1.00	38.38
6792	OWO WAT W 584	46.486	-2.333	51.867	1.00	65.57	6845	OWO WAT W 639	58.636	-8.488	-2.049	1.00	45.41
6793	OWO WAT W 585	76.557	6.773	47.617	1.00	30.60	6846	OWO WAT W 640	51.765	-5.454	-24.427	1.00	30.07
6794	OWO WAT W 586	55.689	0.519	60.810	1.00	37.55	6847	OWO WAT W 641	60.477	-7.078	-5.334	1.00	51.94
6795	OWO WAT W 587	77.597	-7.073	50.855	1.00	44.35	6848	OWO WAT W 642	35.217	24.951	48.021	1.00	36.69
6796	OWO WAT W 588	88.395	-13.032	11.580	1.00	29.59	6849	OWO WAT W 643	25.477	8.964	26.926	1.00	36.50
6797	OWO WAT W 589	41.920	18.111	24.362	1.00	32.25	6850	OWO WAT W 644	73.038	7.145	25.686	1.00	38.10
6798	OWO WAT W 590	37.249	-12.482	31.297	1.00	28.69	6851	OWO WAT W 645	31.546	26.839	42.458	1.00	37.72
6799	OWO WAT W 591	82.022	-21.727	0.851	1.00	41.41	6852	OWO WAT W 646	78.629	5.276	46.680	1.00	31.14
6800	OWO WAT W 592	74.315	9.720	29.056	1.00	36.96	6853	OWO WAT W 647	50.352	-10.415	0.030	1.00	34.69
6801	OWO WAT W 593	51.410	5.026	-6.751	1.00	40.52	6854	OWO WAT W 648	23.075	3.622	57.785	1.00	50.55
6802	OWO WAT W 594	47.526	10.717	59.474	1.00	44.35	6855	OWO WAT W 649	82.155	-23.495	3.245	1.00	34.51
6803	OWO WAT W 595	53.540	-15.820	20.692	1.00	36.01	6856	OWO WAT W 650	53.614	-0.820	-5.533	1.00	30.46
6804	OWO WAT W 596	34.459	-9.857	26.624	1.00	33.62	6857	OWO WAT W 651	41.173	6.120	-12.244	1.00	32.87
6805	OWO WAT W 597	67.159	18.723	29.650	1.00	47.65	6858	OWO WAT W 652	46.461	15.785	29.821	1.00	33.74
6806	OWO WAT W 598	57.902	-6.416	11.043	1.00	36.87	6859	OWO WAT W 653	46.910	-0.266	53.614	1.00	36.78
6807	OWO WAT W 599	33.150	10.072	56.599	1.00	36.61	6860	OWO WAT W 654	54.969	9.457	27.413	1.00	41.28
6808	OWO WAT W 600	80.247	-13.720	45.923	1.00	38.71	6861	OWO WAT W 655	71.413	4.824	11.859	1.00	47.81
6809	OWO WAT W 601	65.256	5.486	60.044	1.00	25.49	6862	OWO WAT W 656	48.713	3.240	-19.259	1.00	36.50
6810	OWO WAT W 602	70.764	-21.357	-4.897	1.00	34.79	6863	OWO WAT W 657	53.539	25.302	32.981	1.00	38.05
6811	OWO WAT W 603	43.485	-13.298	22.439	1.00	36.93	6864	OWO WAT W 658	53.590	-1.475	8.457	1.00	51.45
6812	OWO WAT W 604	55.370	23.838	31.451	1.00	40.61	6865	OWO WAT W 659	79.662	-22.479	-0.183	1.00	50.01
6813	OWO WAT W 605	72.230	-4.477	53.756	1.00	33.63	6866	OWO WAT W 660	18.141	15.650	34.789	1.00	53.01
6814	OWO WAT W 606	86.015	-6.308	44.482	1.00	33.31	6867	OWO WAT W 661	87.154	-0.180	42.783	1.00	47.33
6815	OWO WAT W 607	79.100	6.742	28.261	1.00	36.39	6868	OWO WAT W 662	62.459	9.375	29.050	1.00	30.93
6816	OWO WAT W 608	13.024	10.093	41.592	1.00	39.66	6869	OWO WAT W 663	42.984	25.814	49.065	1.00	34.72
6817	OWO WAT W 610	19.065	2.738	56.666	1.00	36.22	6870	OWO WAT W 664	89.832	-5.536	43.041	1.00	35.89
6818	OWO WAT W 611	27.698	18.474	28.229	1.00	29.78	6871	OWO WAT W 666	95.356	-6.463	30.956	1.00	39.83
6819	OWO WAT W 612	79.524	-22.097	-5.261	1.00	35.00	6872	OWO WAT W 667	70.567	14.899	27.721	1.00	47.74
6820	OWO WAT W 613	78.777	3.843	-0.369	1.00	39.60	6873	OWO WAT W 668	38.060	1.861	56.019	1.00	43.81
6821	OWO WAT W 614	60.674	23.492	32.021	1.00	50.31	6874	OWO WAT W 669	42.573	-12.553	29.782	1.00	44.56
6822	OWO WAT W 615	89.369	-13.520	6.901	1.00	53.93	6875	OWO WAT W 670	63.052	-18.013	29.178	1.00	32.11
6823	OWO WAT W 616	54.674	2.066	-7.514	1.00	35.44	6876	OWO WAT W 671	26.904	-12.528	-19.449	1.00	50.32
6824	OWO WAT W 617	80.241	-21.114	10.183	1.00	45.60	6877	OWO WAT W 672	87.381	-14.602	9.308	1.00	38.68
6825	OWO WAT W 618	39.869	-0.368	53.204	1.00	31.86	6878	OWO WAT W 673	73.626	-6.763	27.221	1.00	44.79
6826	OWO WAT W 619	84.314	0.222	22.029	1.00	38.74	6879	OWO WAT W 674	19.297	10.427	29.648	1.00	53.79
6827	OWO WAT W 620	77.764	-28.451	25.257	1.00	42.43	6880	OWO WAT W 675	61.974	-17.776	43.690	1.00	45.64
6828	OWO WAT W 621	92.860	-6.918	29.400	1.00	43.50	6881	OWO WAT W 676	21.734	16.509	28.603	1.00	52.65
6829	OWO WAT W 623	82.066	-22.011	-5.845	1.00	43.27	6882	OWO WAT W 677	90.154	-12.035	4.840	1.00	52.27
6830	OWO WAT W 624	66.952	21.443	36.324	1.00	35.06	6883	OWO WAT W 678	77.008	5.083	18.362	1.00	38.43
6831	OWO WAT W 625	65.091	-21.080	25.542	1.00	36.11	6884	OWO WAT W 679	78.849	-3.340	8.660	1.00	44.26



6885	OW0	WAT	W	680	37.125	6.546	25.517	1.00	26.76	6938	OW0	WAT	W	733	34.630	6.679	23.929	1.00	43.41
6886	OW0	WAT	W	681	65.476	13.560	57.511	1.00	30.87	6939	OW0	WAT	W	734	57.088	-11.759	-15.829	1.00	40.44
6887	OW0	WAT	W	682	54.416	3.948	15.578	1.00	40.81	6940	OW0	WAT	W	735	79.179	-22.870	6.833	1.00	45.12
6888	OW0	WAT	W	683	53.062	-18.088	22.008	1.00	43.19	6941	OW0	WAT	W	736	38.310	-14.037	35.139	1.00	44.86
6889	OW0	WAT	W	684	12.292	12.538	42.132	1.00	32.07	6942	OW0	WAT	W	737	39.171	-2.907	53.911	1.00	45.60
6890	OW0	WAT	W	685	22.880	9.102	31.205	1.00	44.59	6943	OW0	WAT	W	738	39.322	17.940	52.385	1.00	42.20
6891	OW0	WAT	W	686	24.576	-0.920	55.112	1.00	42.14	6944	OW0	WAT	W	739	48.359	2.635	58.769	1.00	51.66
6892	OW0	WAT	W	687	61.965	-4.738	11.865	1.00	34.12	6945	OW0	WAT	W	740	72.823	5.269	52.825	1.00	45.87
6893	OW0	WAT	W	688	54.878	-16.136	18.394	1.00	42.78	6946	OW0	WAT	W	741	52.762	19.727	28.434	1.00	40.22
6894	OW0	WAT	W	689	16.847	19.568	45.126	1.00	43.60	6947	OW0	WAT	W	742	28.202	-5.793	-6.513	1.00	48.77
6895	OW0	WAT	W	690	55.170	23.039	52.155	1.00	41.75	6948	OW0	WAT	W	743	79.618	1.235	4.432	1.00	42.94
6896	OW0	WAT	W	691	39.834	-12.044	-3.476	1.00	36.25	6949	OW0	WAT	W	744	67.094	-18.257	47.501	1.00	38.02
6897	OW0	WAT	W	692	83.900	-19.454	48.185	1.00	42.85	6950	OW0	WAT	W	745	52.688	10.357	62.956	1.00	40.29
6898	OW0	WAT	W	693	62.276	19.955	30.431	1.00	34.17	6951	OW0	WAT	W	746	40.431	-14.509	-4.481	1.00	42.77
6899	OW0	WAT	W	694	84.970	-6.738	10.835	1.00	42.23	6952	OW0	WAT	W	747	38.750	-10.992	22.885	1.00	44.88
6900	OW0	WAT	W	695	35.725	-14.462	31.165	1.00	39.86	6953	OW0	WAT	W	748	44.292	14.402	59.454	1.00	44.70
6901	OW0	WAT	W	696	58.055	17.975	63.613	1.00	53.19	6954	OW0	WAT	W	749	88.953	-23.063	20.219	1.00	41.34
6902	OW0	WAT	W	697	48.858	27.436	43.339	1.00	47.28	6955	OW0	WAT	W	750	56.054	-11.968	53.046	1.00	60.38
6903	OW0	WAT	W	698	63.336	-8.234	57.236	1.00	47.00	6956	OW0	WAT	W	751	41.969	29.748	47.846	1.00	20.50
6904	OW0	WAT	W	699	70.147	-26.087	29.342	1.00	55.27	6957	OW0	WAT	W	752	44.966	-16.181	23.899	1.00	50.48
6905	OW0	WAT	W	700	66.692	-14.096	-16.368	1.00	45.91	6958	OW0	WAT	W	753	85.644	-22.932	2.568	1.00	43.55
6906	OW0	WAT	W	701	40.692	15.224	56.764	1.00	46.42	6959	OW0	WAT	W	754	43.034	6.314	-21.514	1.00	51.86
6907	OW0	WAT	W	702	79.719	-28.791	22.760	1.00	32.02	6960	OW0	WAT	W	755	84.872	4.181	42.842	1.00	49.44
6908	OW0	WAT	W	703	59.465	21.759	30.551	1.00	42.42	6961	OW0	WAT	W	756	74.363	11.696	34.959	1.00	37.97
6909	OW0	WAT	W	704	31.141	-5.131	22.552	1.00	68.52	6962	OW0	WAT	W	757	80.803	5.977	33.052	1.00	43.23
6910	OW0	WAT	W	705	36.695	-16.973	-4.878	1.00	37.89	6963	OW0	WAT	W	758	61.280	17.301	58.888	1.00	40.96
6911	OW0	WAT	W	706	80.687	-20.765	47.298	1.00	38.30	6964	OW0	WAT	W	759	35.859	19.793	23.282	1.00	48.10
6912	OW0	WAT	W	707	54.669	3.010	-9.815	1.00	46.05	6965	OW0	WAT	W	760	20.148	19.237	32.614	1.00	31.76
6913	OW0	WAT	W	708	43.216	-8.260	47.123	1.00	40.03	6966	OW0	WAT	W	761	15.289	11.762	36.214	1.00	43.45
6914	OW0	WAT	W	709	70.862	15.600	41.973	1.00	37.00	6967	OW0	WAT	W	762	46.595	-5.917	-22.133	1.00	44.31
6915	OW0	WAT	W	710	33.412	-2.522	54.114	1.00	48.11	6968	OW0	WAT	W	763	20.413	11.283	60.057	1.00	50.11
6916	OW0	WAT	W	711	92.535	-0.923	34.738	1.00	49.47	6969	OW0	WAT	W	764	68.167	5.712	13.653	1.00	30.67
6917	OW0	WAT	W	712	33.025	23.917	47.317	1.00	46.24	6970	OW0	WAT	W	765	54.184	2.615	-12.252	1.00	39.38
6918	OW0	WAT	W	713	70.249	17.850	37.204	1.00	40.78	6971	OW0	WAT	W	766	84.664	-22.555	14.359	1.00	45.78
6919	OW0	WAT	W	714	41.368	22.495	53.675	1.00	40.32	6972	OW0	WAT	W	767	30.072	-20.212	-10.959	1.00	38.35
6920	OW0	WAT	W	715	76.578	-19.899	49.657	1.00	40.87	6973	OW0	WAT	W	768	41.072	-0.946	-21.837	1.00	41.66
6921	OW0	WAT	W	716	90.425	-4.420	30.203	1.00	60.30	6974	OW0	WAT	W	769	61.874	11.916	27.798	1.00	44.81
6922	OW0	WAT	W	717	34.487	19.062	20.833	1.00	45.89	6975	OW0	WAT	W	770	66.356	5.178	-1.773	1.00	65.15
6923	OW0	WAT	W	718	89.801	-4.016	22.869	1.00	46.61	6976	OW0	WAT	W	771	26.844	5.186	59.968	1.00	46.27
6924	OW0	WAT	W	719	74.377	1.047	-13.486	1.00	51.80	6977	OW0	WAT	W	772	36.878	24.305	28.318	1.00	34.70
6925	OW0	WAT	W	720	66.403	4.257	9.718	1.00	41.97	6978	OW0	WAT	W	773	54.912	-1.550	-21.819	1.00	42.64
6926	OW0	WAT	W	721	56.444	-17.979	-12.402	1.00	40.83	6979	OW0	WAT	W	774	59.594	-17.858	41.366	1.00	37.27
6927	OW0	WAT	W	722	82.588	-0.182	1.654	1.00	55.22	6980	OW0	WAT	W	775	57.520	-15.150	18.294	1.00	36.30
6928	OW0	WAT	W	723	61.949	-0.825	-0.993	1.00	44.85	6981	OW0	WAT	W	776	32.998	24.523	34.342	1.00	42.23
6929	OW0	WAT	W	724	94.665	-3.882	41.279	1.00	43.45	6982	OW0	WAT	W	777	59.020	-12.114	56.789	1.00	57.61
6930	OW0	WAT	W	725	78.637	-22.418	46.944	1.00	49.42	6983	OW0	WAT	W	778	81.113	-27.278	43.621	1.00	41.79
6931	OW0	WAT	W	726	76.801	0.776	11.150	1.00	43.15	6984	OW0	WAT	W	779	73.319	-20.756	38.654	1.00	43.17
6932	OW0	WAT	W	727	36.682	26.179	34.703	1.00	46.16	6985	OW0	WAT	W	780	75.478	-16.566	37.845	1.00	51.42
6933	OW0	WAT	W	728	52.946	-24.152	35.886	1.00	42.32	6986	OW0	WAT	W	781	91.610	-6.042	15.770	1.00	36.38
6934	OW0	WAT	W	729	44.065	-10.820	0.741	1.00	58.49	6987	OW0	WAT	W	782	71.605	16.644	39.410	1.00	48.62
6935	OW0	WAT	W	730	59.442	-15.580	42.690	1.00	31.69	6988	OW0	WAT	W	783	63.508	24.207	41.029	1.00	44.22
6936	OW0	WAT	W	731	72.384	8.537	51.566	1.00	31.82	6989	OW0	WAT	W	784	88.822	-11.109	7.822	1.00	48.78
6937	OW0	WAT	W	732	31.347	-6.053	26.265	1.00	42.64	6990	OW0	WAT	W	785	71.691	-23.906	33.801	1.00	48.29

6991	OWO	WAT	W	786	52.032	8.913	29.301	1.00	39.41	7044	OWO	WAT	W	839	23.969	-18.104	-13.469	1.00	44.44
6992	OWO	WAT	W	787	72.141	14.023	31.846	1.00	37.55	7045	OWO	WAT	W	840	98.275	-11.384	39.798	1.00	40.16
6993	OWO	WAT	W	788	39.138	16.149	26.862	1.00	50.27	7046	OWO	WAT	W	841	43.468	-4.550	50.159	1.00	42.27
6994	OWO	WAT	W	789	37.813	-9.039	47.875	1.00	13.18	7047	OWO	WAT	W	842	55.531	24.997	41.758	1.00	43.49
6995	OWO	WAT	W	790	35.173	-8.363	50.198	1.00	39.87	7048	OWO	WAT	W	843	79.423	-25.689	-0.377	1.00	50.83
6996	OWO	WAT	W	791	26.847	-1.258	31.548	1.00	39.21	7049	OWO	WAT	W	844	82.729	-5.447	14.530	1.00	37.55
6997	OWO	WAT	W	792	88.614	-23.766	1.624	1.00	54.25	7050	OWO	WAT	W	845	57.277	-20.688	32.754	1.00	27.47
6998	OWO	WAT	W	793	21.121	7.089	31.169	1.00	50.12	7051	OWO	WAT	W	846	34.927	18.980	47.765	1.00	43.87
6999	OWO	WAT	W	794	41.636	21.622	50.969	1.00	47.76	7052	OWO	WAT	W	847	66.697	21.490	33.750	1.00	55.52
7000	OWO	WAT	W	795	26.421	0.362	29.613	1.00	43.60	7053	OWO	WAT	W	848	52.866	-18.940	42.635	1.00	48.02
7001	OWO	WAT	W	796	44.401	-8.843	23.747	1.00	40.62	7054	OWO	WAT	W	849	50.290	-12.920	19.561	1.00	49.79
7002	OWO	WAT	W	797	70.057	18.053	42.138	1.00	38.55	7055	OWO	WAT	W	850	24.446	5.767	29.203	1.00	39.68
7003	OWO	WAT	W	798	66.270	-17.604	-6.916	1.00	45.58	7056	OWO	WAT	W	851	44.555	9.373	55.910	1.00	40.43
7004	OWO	WAT	W	799	46.164	31.367	45.417	1.00	51.35	7057	OWO	WAT	W	852	59.190	7.201	65.033	1.00	43.41
7005	OWO	WAT	W	800	75.137	5.508	51.679	1.00	45.47	7058	OWO	WAT	W	853	23.010	7.765	61.451	1.00	52.83
7006	OWO	WAT	W	801	18.046	3.941	59.147	1.00	42.23	7059	OWO	WAT	W	854	22.922	24.189	36.031	1.00	41.20
7007	OWO	WAT	W	802	59.339	0.402	-2.076	1.00	52.88	7060	OWO	WAT	W	855	57.790	-3.694	56.332	1.00	51.83
7008	OWO	WAT	W	803	55.564	-18.287	-15.179	1.00	38.85	7061	OWO	WAT	W	856	23.937	14.064	59.101	1.00	46.09
7009	OWO	WAT	W	804	28.418	0.009	26.267	1.00	52.59	7062	OWO	WAT	W	857	65.116	20.932	49.254	1.00	41.13
7010	OWO	WAT	W	805	97.132	-12.269	27.826	1.00	38.21	7063	OWO	WAT	W	858	38.488	17.732	55.214	1.00	40.12
7011	OWO	WAT	W	806	21.485	21.769	33.106	1.00	37.99	7064	OWO	WAT	W	859	39.060	7.114	-23.052	1.00	31.07
7012	OWO	WAT	W	807	61.494	-16.277	-11.458	1.00	32.24	7065	OWO	WAT	W	860	44.261	9.954	-10.440	1.00	45.44
7013	OWO	WAT	W	808	77.944	-0.349	8.828	1.00	56.65										

## APPENDIX 2

Promozyyme	1	DSTSTKVIHV	YHRFDSNYTN	WDVMMWPYQP	VNGNGAAYQF	TGTNDDFGAV	50
B.acidopul		DSTSTEVIHV	YHRFDSNYAN	WDLMMWPYQP	VNGNGAAYEF	SG.KDDDFGVK	
B.deramifi		DGNTTTIIVH	YFRPAGDYQP	WSLMMW...P	KDGGGAHEYDF	NQPADSFGAV	
Promozyyme	51	ADTQVPGDNT	QVGLIVRKND	WSEKNTPNDL	HIDLAKGHEV	WIVQGDPTIY	100
B.acidopul		ADVQVPGDDT	QVGLIVRTND	WSQKNTSDDL	HIDLTGKHEI	WIVQGDPNIY	
B.deramifi		ASADIPGNPS	QVGIIIVRTQD	WT.KDVSADR	YIDLKSGNEV	WLVEGNSQIF	
Promozyyme	101	YNLSDAQAAA	IPSVSNAYLD	DEKTVLAKLS	MPMTLADAAS	GFTVIDKTTG	150
B.acidopul		YNLSDAQAAA	TPKVSNAAYLD	NEKTVLAKLT	NPMTLSDGSS	GFTVTDKTTG	
B.deramifi		YNEKDAEDAA	KPAVSNAAYLD	ASNQVLVKLS	QPLTLGEGAS	GFTVHDDTAN	
Promozyyme	151	EKIPVTSAVS	A...NPVTAV	LVGDLQQALG	AANNWSPDDD	HTLLKKINPN	197
B.acidopul		EQIPVTAATN	A...NS....	.....	.....	.....	
B.deramifi		KDIPVTSVKD	ASLGQDVTAV	LAGTFQHIFG	GS.DWAPDNH	STLLKKVTNN	
Promozyyme	198	LYQLSGTLPA	GTYYQKIALD	HSW.NTSYPG	NNVSLTVPOG	GEKVTFTYIP	246
B.acidopul		.....	.....	.....	.....	.....	
B.deramifi		LYQFSGDLPE	GNYYQKVALN	DSWNNPSYPS	DNINLTVPAG	GAHVTFYSYIP	
Promozyyme	247	STNQVFDSVN	HPNQAFPTSS	AGVQTNLVQL	TLASAPDVTH	NLDVAADGYK	296
B.acidopul		.....	.....AS	SSEQTDLVQL	TLASAPDVSH	TIQVGAAGYE	
B.deramifi		STHAVYDTIN	NPNADLQVES	.GVKTDLVTV	TLGEDPDVSH	TLSIQTDGYQ	
Promozyyme	297	AHNILPRNVL	NLPRYDYSN	DLGNVYSKDA	TSFRVWAPTA	SNVQLLLYNS	346
B.acidopul		AVNLIPRNVL	NLPRYYSN	DLGNVYSNKA	TAFRVWAPTA	SDVQLLLYNS	
B.deramifi		AKQVIPRNVL	NSSQYYYSN	DLGNTYTQKA	TTFKVWAPTS	TQVNVLLYDS	
Promozyyme	347	EKGSITKQLE	MQKSDNGTWK	LQVSCNLENW	YYLYQVTVNG	TTQTAVDPYA	396
B.acidopul		ETGPVTKQLE	MQKSDNGTWK	LKVPGNLKNW	YYLYQVTVNG	KTQTAVDPYV	
B.deramifi		ATGSVTKIVP	MTASGHGVWE	ATVNQNLENW	YYMYEVTGQG	STRTAVDPYA	
Promozyyme	397	RAISVNATRG	MIVDLKATDP	AGWQGDHEQT	PANPVDEVIY	EAHVRDFSID	446
B.acidopul		RAISVNATRG	MIVDLEDTP	PGWKEDHQQT	PANPVDEVIY	EVHVRDFSID	
B.deramifi		TAIAPNGTRG	MIVDLAKTDP	AGWNSDKHIT	PKNIEDEVIY	EMDVRDFSID	
Promozyyme	447	ANSGMKNKGK	YLAFTEHGK	GPDHVKTGID	SLKELGITT	QLQPVEEFNS	496
B.acidopul		ANSGMKNKGK	YLAFTEHGK	GPDNVKTGID	SLKELGINAV	QLQPIEEFNS	
B.deramifi		PNSGMKNKGK	YLALTEKGK	GPDNVKTGID	SLKQLGITHV	QLMPVFASNS	
Promozyyme	497	IDETQPDYTN	WGYDPRNINV	PEGAYATTPE	GTARITELKQ	LIQSLHQQRI	546
B.acidopul		IDETQPNMYN	WGYDPRNINV	PEGAYATTPE	GTARITQLKQ	LIQSIHKDRI	
B.deramifi		VDETDPTQDN	WGYDPRNYDV	PEGQYATNAN	GNARIKEFKE	MVLSLHREHI	

	547				596
Promozyyme	GVNMDVVYNH	TFDVMVSDFD	KIVPQYYYRT	DSNGNYTNGS	GCGNEFATEH
B.acidopul	AINMDVVYNH	TFNVGVSDFD	KIVPQYYYRT	DSAGNYTNGS	GVGNEIATER
B.deramifi	GVNMDVVYNH	TFATQISDFD	KIVPEYYYRT	DDAGNYTNGS	GTGNEIAAER
	597				646
Promozyyme	PMAQKFVLDS	VNYWVNEYHV	DGFRFDLMAL	LGKDTMAKIS	NELHAINPGI
B.acidopul	PMVQKFVLDS	VKYWVKEYHI	DGFRFDLMAL	LGKDTMAKIS	KELHAINPGI
B.deramifi	PMVQKFIIDS	LKYWVNEYHI	DGFRFDLMAL	LGKDTMSKAA	SELHAINPGI
	647				696
Promozyyme	VLYGEPWTGG	TSGLSSDQLV	TKGQQKGLGI	GVFNDNIRNG	LDGNVFDKTA
B.acidopul	VLYGEPWTGG	TSGLSSDQLV	TKGQQKGLGI	GVFNDNIRNG	LDGNVFDKSA
B.deramifi	ALYGEPWTGG	TSALPDDQLL	TKGAQKGMGV	AVFNDNLRNA	LDGNVFDSSA
	697				746
Promozyyme	QGFATGDPNQ	VDVIKNGVIG	SIQDFTSAPS	ETINYVTSHD	NMTLWDKILA
B.acidopul	QGFATGDPNQ	VNVIKNRVMG	SISDFTSAPS	ETINYVTSHD	NMTLWDKISA
B.deramifi	QGFATGATGL	TDAIKNGVEG	SINDFTSSPG	ETINYVTSHD	NYTLWDKIAL
	747				796
Promozyyme	SNPSDTEADR	IKMDELAHAV	VFTSQGVPFM	QGGEMLRTK	GGNDNSYNAG
B.acidopul	SNPNDTQADR	IKMDELAQAV	VFTSQGVPFM	QGGEMLRTK	GGNDNSYNAG
B.deramifi	SNPNDEADR	IKMDELAQAV	VMTSQGVPFM	QGGEMLRTK	GGNDNSYNAG
	797				846
Promozyyme	DSVNQFDWSR	KAQFKDVFYD	FSSMIHLRNQ	HPAFRMTTAD	QIKQNLTFLE
B.acidopul	DSVNQFDWSR	KAQFENVFDY	YSWLIHLRDN	HPAFRMTTAD	QIKQNLTFLD
B.deramifi	DAVNEFDWSR	KAQYPDVFN	YSGLIHLRLD	HPAFRMTTAN	EINSHLQFLN
	847				896
Promozyyme	SPTNTVAFEL	KNYANHDTWK	NIIVMYNPNK	TSQTLNLPSP	DWTIVGLGDQ
B.acidopul	SPTNTVAFEL	KNHANHDKWK	NIIVMYNPNK	TAQTLTLPSP	NWTIVGLGNQ
B.deramifi	SPENTVAYEL	TDHVNKDKWG	NIIVVYNPNK	TVATINLPSP	KWAINATSGK
	897		921		
Promozyyme	IGEKSLSGHVM	GNVQVPAIST	LILKQ.....	.....	
B.acidopul	VGEKSLSGHVN	GTVEVPALST	IILHQGTSED	VIDQN	
B.deramifi	VGESTLGQAE	GSVQVPGISM	MILHQEVSPD	HGKK.	